

STIC-Biotech/ChemLib

167633

From: Foley, Shanon
Sent: Tuesday, October 04, 2005 9:03 AM
To: STIC-Biotech/ChemLib
Subject: Database Search Request

Requester:
Shanon Foley (TC1600)
Art Unit:
1648
Employee Number:
77851
Office Location:
3C21
Phone Number:
2-0898
Mailbox Number:

RECEIVED
OCT -4 2005
STIC-Biotech/ChemLib
(STIC)

Case serial number:
10/694247
Class / Subclass(es):

Earliest Priority Filing Date:

Format preferred for results:
Paper

Search Topic Information:

Please search amino acid SEQ ID NO: 2. I am interested in anything that has at least 70% sequence identity with this sequence. Please expand hit list as appropriate so that all relevant answers are listed. If the list is unusually, large, please put the results on a disc.

Thank you.
Special Instructions and Other Comments:

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: 10/5
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 5, 2005, 10:03:10 ; Search time 166 Seconds
(without alignments)
400.740 Million cell updates/sec

Title: US-10-694-247-2
Perfect score: 907
Sequence: 1 CYSRKLMDARENLKILDR.....TVSTTLQKRLTKRGDLNSP 172

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database :

1: A_GeneSeq_16Dec04:*
2: geneeqp19808:*
3: geneeqp19908:*
4: geneeqp20018:*
5: geneeqp20028:*
6: geneeqp20038:*
7: geneeqp20048:*
8: geneeqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	907	100.0	172	2	AAR54768 Sheep int
2	907	100.0	172	2	AAR9397 Ovine tau
3	907	100.0	172	2	AAM31698 Mature ov
4	907	100.0	172	2	AAM44110 Mature ov
5	907	100.0	172	5	ABBO7588 Ovine int
6	907	100.0	172	7	AD117857 Mature int
7	907	100.0	172	8	ADM79177 Mature ov
8	907	100.0	172	8	AD131613 Sheep int
9	907	100.0	172	2	AAR04540 Ovine tro
10	905	99.8	172	2	AAR09294 Ovine tro
11	905	99.8	172	8	ADM79195 Interfero
12	904	99.7	195	2	AAR24942 Sequence
13	900	99.2	172	4	AAB31457 Amino aci
14	900	99.2	172	5	AAO21461 Ovine int
15	899	99.1	172	5	ABBO7589 Recombina
16	899	99.1	172	8	ADM79178 Mature ov
17	899	99.1	172	4	AD131614 Recombina
18	898	99.0	172	4	AAB31462 An ovine
19	897	98.9	195	2	AAR24941 Sequence
20	897	98.9	195	2	AAR24945 Sequence
21	896	98.8	172	4	AAB31468 An ovine
22	896	98.8	172	4	AAB31466 An ovine
23	896	98.8	172	4	AAB31464 An ovine
24	895	98.7	172	4	AAB31459 An ovine
25	894	98.6	172	4	AAB31467 An ovine

26	894	98.6	172	4	AAB31465 An ovine
27	894	98.6	172	4	AAB31460 An ovine
28	894	98.6	172	4	AAR24944 Sequence
29	892	98.3	172	4	AAB31461 An ovine
30	890	98.1	172	4	AAB31463 An ovine
31	883	97.4	195	1	AAP91396 Isoform o
32	874	96.4	195	2	AAR24943 Sequence
33	857.5	94.5	196	4	AAB49784 Ovi TP-1
34	857.5	94.5	196	7	ADP94976 Sheep IFN
35	786	86.7	152	8	AD131633 Human int
36	723	79.7	195	8	AAB49783 Bovine TP
37	723	79.7	195	5	ABBO8641 Bovine in
38	723	79.7	195	5	ADP94975 Bovine IF
39	720	79.4	195	2	AAR04539 Bovine IF
40	691	76.2	173	2	AAM70809 A tau mod
41	649	71.6	171	7	ADG42697 Human int
42	649	71.6	171	7	ADJ55766 Peptide h
43	649	71.6	171	8	ADM76604 Human NOV
44	647	71.3	173	2	AAM70808 A tau mod
45	632	69.7	173	2	AAM56435 Amino aci
46	632	69.7	173	2	AAM70814 A human i
47	628	69.2	173	2	AAM56433 Amino aci
48	628	69.2	173	2	AAM70812 A human i
49	627	69.1	173	2	AAM56434 Amino aci
50	627	69.1	173	2	AAM70813 A human i
51	621	68.5	173	2	AAM56437 Amino aci
52	615	67.8	173	2	AAM56440 Amino aci
53	614	67.7	173	2	AAM56439 Amino aci
54	612	67.5	172	2	AAM09278 Human mat
55	612	67.5	172	2	AAR93938 Human tau
56	612	67.5	172	2	AAM31699 Human int
57	612	67.5	172	2	AAM44111 Synthetic
58	612	67.5	172	2	AAM44117 Mature hu
59	612	67.5	173	2	AAM70811 A human i
60	612	67.5	195	2	AAM09288 Human com
61	612	67.5	195	2	AAM44106 Human int
62	611	67.4	173	2	AAM74460 Human int
63	609	67.1	172	2	AAR54769 Human int
64	609	67.1	172	2	AAM09277 Human mat
65	609	67.1	172	4	AAB49169 Human int
66	609	67.1	173	2	AAM56438 Amino aci
67	609	67.1	173	2	AAM56436 Amino aci
68	609	67.1	173	2	AAM70810 Amino aci
69	609	67.1	195	2	AAR54770 Human int
70	604	66.6	171	2	AAM09279 Human mat
71	604	66.6	171	2	AAM44116 Human int
72	600.5	66.2	194	4	AAB49777 Human pla
73	600.5	66.2	194	7	ADP94969 Human pla
74	599	66.0	172	2	AAM09281 Human mat
75	599	66.0	172	2	AAR93939 Human tau
76	599	66.0	172	2	AAM31700 Human int
77	599	66.0	172	2	AAM44108 Mature hu
78	599	66.0	173	2	AAM74461 Human int
79	599	66.0	195	2	AAM09289 Human com
80	599	66.0	195	2	AAM44107 Human int
81	596	65.7	172	2	AAM09280 Human mat
82	582	64.2	195	1	AAP30076 Sequence
83	582	64.2	195	2	AAM73227 Bovine in
84	582	64.2	195	2	AAM83898 Bovine in
85	582	64.2	195	5	ABG32983 Bovine le
86	576	63.5	195	2	AAR04541 Bovine in
87	525	57.9	172	2	AAM09276 Human mat
88	521	57.4	166	8	ADM79185 Human int
89	518	57.1	166	8	AAY05806 Human int
90	518	57.1	166	8	ADM79188 Interfero
91	510	56.2	166	8	ADM79186 Interfero
92	502	55.3	166	2	AAY05810 Human int
93	502	55.3	166	8	ADM79192 Interfero
94	498	54.9	166	2	AAY05811 Human int
95	498	54.9	166	8	ADM79193 Interfero
96	489	53.9	195	1	AAP60403 Equine IF
97	484	53.4	166	2	AAY05809 Human int
98	484	53.4	166	8	ADM79191 Interfero

99	481	53.0	172	6	ABP96600	Hybrid	int				
100	479	52.8	166	2	AAy05812	Human	int				
101	479	52.8	166	8	ADm79194	Interfero					
102	473	52.1	172	4	AbA49170	Human	int				
103	473	52.1	173	1	AAp70330	Sequence					
104	473	52.1	195	1	AAp60253	Interfero					
105	473	52.1	195	2	AAp66198	E.coli ST					
106	473	52.1	195	2	AAy22635	Human	int				
107	473	52.1	195	3	AAAB13433	Human	int				
108	473	52.1	195	5	ABBO7439	Interfero					
109	473	52.1	195	5	ADm13727	Human	int				
110	473	52.1	195	8	ADN10817	Human	int				
111	473	52.1	195	8	ADN49747	Human	int				
112	473	52.1	195	8	ADs16327	Human	int				
113	473	52.1	352	5	ABBO5344	Human	int				
114	473	52.1	350	7	ADD69668	Chimeric					
115	467	51.5	166	2	AAy05808	Human	int				
116	467	51.5	166	8	ADm79190	Interfero					
117	465	51.3	195	4	AAp60355	Sequence					
118	465	51.3	195	4	AAAB49781	Human	int				
119	465	51.3	195	7	ADP94973	Human	int				
120	464	51.2	162	2	AAy25093	Human	int				
121	461	50.8	195	2	AAw53120	Amrino act					
122	460.5	50.8	171	1	AAp70332	Sequence					
123	460.5	50.8	172	2	AAAR24030	Human	int				
124	459.5	50.7	172	2	AAAR24031	Human	int				
125	456	50.3	166	2	AAy05813	Human	int				
126	456	50.3	166	6	AAg79719	IFN-alpha					
127	456	50.3	166	8	ADm79187	Interfero					
128	453	49.9	166	4	AAAG61804	Interfero					
129	453	49.9	166	8	AD129632	Human	int				
130	451	49.7	167	1	AAp70442	Sequence					
131	448	49.4	166	2	AAy05807	Human	int				
132	448	49.4	166	8	ADm79189	Interfero					
133	446	49.2	176	1	AAp60557	Interfero					
134	445	49.1	182	1	AAp30003	Sequence					
135	444	49.0	195	1	AAp60400	Equine IF					
136	442	48.7	166	4	AAAG61797	Interfero					
137	442	48.7	166	4	AAAG61828	Interfero					
138	442	48.7	166	5	ABG68078	Human	int				
139	442	48.7	166	8	AD129625	Human	int				
140	442	48.7	166	8	AD129663	Human	int				
141	442	48.7	167	2	AAAR11532	Consensus					
142	442	48.7	189	5	ABG68070	Human	int				
143	441	48.6	166	4	AAAG61805	Interfero					
144	441	48.6	166	8	AD129633	Human	int				
145	440	48.5	166	1	AAp60304	Sequence					
146	440	48.5	166	4	AAAR67761	Interfero					
147	440	48.5	166	4	AAAB49160	Human	int				
148	440	48.5	166	4	AAAG61803	Interfero					
149	440	48.5	166	8	AD129631	Human	int				
150	440	48.5	166	8	ADL88859	Human	cyt				
151	440	48.5	166	8	ADL88853	Human	cyt				
152	440	48.5	166	8	AD032377	Human	int				
153	440	48.5	167	1	AAp30231	Sequence					
154	440	48.5	167	1	AAp30224	Sequence					
155	440	48.5	167	1	AAp60690	E.coli					
156	440	48.5	167	2	AAAR07679	IFN-alpha					
157	440	48.5	189	2	AAAR07678	IFN-alpha					
158	440	48.5	189	5	AAAW70371	Human	int				
159	440	48.5	189	5	ABBO7431	Interfero					
160	440	48.5	189	5	AAAG78572	Human	int				
161	440	48.5	189	6	ABP70735	Human	int				
162	440	48.5	189	7	ADG64979	Interfero					
163	440	48.5	189	8	ADN10804	Human	int				
164	440	48.5	189	8	ADs16314	Human	int				
165	440	48.5	245	7	ADP94970	Human	int				
166	440	48.5	245	7	ADP94970	Human	int				
167	438	48.3	166	4	AAAB49167	Human	int				
168	438	48.3	166	4	AAAG61819	Interfero					
169	438	48.3	166	4	AAAG61792	Interfero					
170	438	48.3	166	4	AAAG61824	Interfero					
171	438	48.3	166	4	AAAG61795	Interfero					
172	438	48.3	172	438	438	48.3	166	8	AD129652	Human	int
173	438	48.3	173	438	438	48.3	166	8	AD129623	Human	int
174	438	48.3	175	438	438	48.3	166	8	AD129620	Human	int
175	438	48.3	176	438	438	48.3	166	8	AD129647	Human	int
176	438	48.3	177	438	438	48.3	166	8	ADL88857	Human	cyt
177	438	48.3	178	438	438	48.3	166	8	AD032386	Human	int
178	438	48.3	178	438	438	48.3	166	8	AD032384	Human	int
179	438	48.3	179	438	438	48.3	167	2	AAAR11531	Consensus	
180	438	48.3	180	438	438	48.3	167	8	AD081759	IFN-co.	
181	438	48.3	181	438	438	48.3	167	8	ADAR97080	Consensus	
182	438	48.3	182	438	438	48.3	167	8	ADAR87295	Consensus	
183	438	48.3	183	438	438	48.3	189	5	AAAG78567	Human	int
184	438	48.3	184	438	438	48.3	189	6	AAAE14832	Human	int
185	438	48.3	185	438	438	48.3	189	6	AAAE14830	Human	int
186	438	48.3	186	438	438	48.3	189	7	ADN13719	Human	int
187	438	48.3	187	438	438	48.3	189	8	ADN10812	Human	int
188	438	48.3	188	438	438	48.3	189	8	ADs16322	Human	int
189	437	48.2	189	437	437	48.2	166	3	AAAB28177	Chimeric	
190	437	48.2	190	437	437	48.2	166	4	AAAG61794	Interfero	
191	437	48.2	191	437	437	48.2	166	4	AAAG61794	Interfero	
192	437	48.2	192	437	437	48.2	189	6	ABP70736	Human	int
193	436	48.1	193	436	436	48.1	166	1	AAAP30685	Consensus	
194	436	48.1	194	436	436	48.1	170	4	AAAB49165	Human	int
195	436	48.1	195	436	436	48.1	189	1	AAAP20110	Sequence	
196	436	48.1	196	436	436	48.1	189	1	AAAP30230	Sequence	
197	436	48.1	197	436	436	48.1	189	5	ABBO7436	Interfero	
198	436	48.1	198	436	436	48.1	189	8	ADN10810	Human	int
199	436	48.1	199	436	436	48.1	189	8	ADs16320	Human	int
200	435	48.0	200	435	435	48.0	166	3	AAAB28176	Human	int
201	435	48.0	201	435	435	48.0	166	4	AAAG61814	Interfero	
202	435	48.0	202	435	435	48.0	166	4	AAAG61793	Interfero	
203	435	48.0	203	435	435	48.0	166	8	AD129621	Human	int
204	435	48.0	204	435	435	48.0	166	8	AD129642	Human	int
205	435	48.0	205	435	435	48.0	171	7	ADP47855	Human	int
206	435	48.0	206	435	435	48.0	189	5	ABG68069	Human	int
207	434	47.9	207	434	434	47.9	166	4	AAAG61818	Interfero	
208	434	47.9	208	434	434	47.9	166	8	AD129646	Human	int
209	433	47.7	209	433	433	47.7	166	2	AAW44105	Chimeric	
210	433	47.7	210	433	433	47.7	166	4	AAAG61802	Interfero	
211	433	47.7	211	433	433	47.7	166	4	AAAG61831	Interfero	
212	433	47.7	212	433	433	47.7	166	4	AAAG61832	Interfero	
213	433	47.7	213	433	433	47.7	166	4	AAAG61790	Interfero	
214	433	47.7	214	433	433	47.7	166	4	AAAG61823	Interfero	
215	433	47.7	215	433	433	47.7	166	4	AAAG61799	Interfero	
216	433	47.7	216	433	433	47.7	166	5	ABG68838	Interfero	
217	433	47.7	217	433	433	47.7	166	8	AD129627	Human	int
218	433	47.7	218	433	433	47.7	166	8	AD129651	Human	int
219	433	47.7	219	433	433	47.7	166	8	AD129630	Human	int
220	433	47.7	220	433	433	47.7	166	8	AD129618	Human	int
221	433	47.7	221	433	433	47.7	166	8	AD129666	Human	int
222	433	47.7	222	433	433	47.7	166	8	AD129667	Human	int
223	433	47.7	223	433	433	47.7	166	8	AD032382	Human	int
224	433	47.7	224	433	433	47.7	189	1	AAAP10021	Sequence	
225	432	47.6	225	432	432	47.6	166	1	AAAP30684	Consensus	
226	432	47.6	226	432	432	47.6	166	4	AAAG619154	Human	int
227	432	47.6	227	432	432	47.6	166	4	AAAG61830	Interfero	
228	432	47.6	228	432	432	47.6	166	4	AAAG61812	Interfero	
229	432	47.6	229	432	432	47.6	166	8	AD129640	Human	int
230	432	47.6	230	432	432	47.6	166	8	AD129665	Human	int
231	432	47.6	231	432	432	47.6	167	2	AAAR11533	Consensus	
232	432	47.5	232	432	432	47.5	238	4	AAAB49775	Human	int
233	431	47.5	233	431	431	47.5	238	7	ADP94967	Human	int
234	430	47.4	234	430	430	47.4	167	1	AAAP30218	Sequence	
235	430	47.4	235	430	430	47.4	167	1	AAPE0686	Sequence	
236	430	47.4	236	430	430	47.4	189	1	AAPE20106	Sequence	
237	430	47.4	237	430	430	47.4	189	6	ABP70737	Human	int
238	429	47.3	238	429	429	47.3	166	4	AAAB49159	Human	int
239	429	47.3	239	429	429	47.3	166	4	AAAB49164	Human	int
240	429	47.3	240	429	429	47.3	166	4	AAAG61796	Interfero	
241	429	47.3	241	429	429	47.3	166	8	AD129624	Human	int
242	429	47.3	242	429	429	47.3	166	8	ADL88856	Human	cyt
243	429	47.3	243	429	429	47.3	166	8	ADL88849	Human	cyt
244	429	47.3	244	429	429	47.3	166	8	AD032381	Human	int

245	429	47.3	166	8	ADO32376	Ado32376	Human	int	318	424	46.7	166	4	AAAG61817	Aag61817	Interfero
246	429	47.3	167	1	AAP30229	Aap30229	Sequence		319	424	46.7	166	8	AD129645	Ad129645	Human
247	429	47.3	167	1	AAP80046	Aap80046	Sequence		320	424	46.7	166	8	ADO32445	Ado32445	Human
248	429	47.3	189	1	AAP20105	Aap20105	Sequence		321	424	46.7	166	8	ADO32351	Ado32351	Human
249	429	47.3	189	1	AAP30228	Aap30228	Sequence		322	424	46.7	167	1	AAP40129	Aap40129	Sequence
250	429	47.3	189	5	ABBO7432	Abb07432	Interfero		323	424	46.7	189	5	ABG68061	Abg68061	Human
251	429	47.3	189	5	ABBO7438	Abb07438	Interfero		324	423	46.6	166	1	AAP60828	Aap60828	Sequence
252	429	47.3	189	5	AAAG7856	Aag7856	Human	int	325	423	46.6	166	4	AAAG61811	Aag61811	Interfero
253	429	47.3	189	5	AAAG7856	Aag7856	Human	int	326	423	46.6	166	8	AD129639	Ad129639	Human
254	429	47.3	189	8	ADN10808	Adn10808	Human	int	327	423	46.6	166	8	ADO32447	Ado32447	Human
255	429	47.3	189	8	ADSL16318	Adsl6318	Human	int	328	423	46.6	189	1	AAP30165	Aap30165	Sequence
256	428	47.2	166	1	AAP50229	Aap50229	Interfero		329	423	46.6	189	4	AAAB49779	Aab49779	Human
257	428	47.2	166	2	AAAR42813	Aar42813	Lymphobla		330	423	46.6	189	7	ADPF94971	Adf94971	Human
258	428	47.2	166	2	AAAM43380	Aam43380	Human	int	331	422	46.5	166	4	AAAG61810	Aag61810	Interfero
259	428	47.2	166	3	AAAB07339	Aab07339	Matucre	hu	332	422	46.5	166	4	AAAG61826	Aag61826	Interfero
260	428	47.2	166	3	AAAY44831	Aay44831	Hybrid	in	333	422	46.5	166	4	AAAG61816	Aag61816	Interfero
261	428	47.2	166	3	AAAB12968	Aab12968	Human	int	334	422	46.5	166	4	AAAE14365	Aae14365	Human
262	428	47.2	166	4	AAAB49157	Aab49157	Human	int	335	422	46.5	166	5	ABG68077	Abg68077	Human
263	428	47.2	166	4	AAAG61800	Aag61800	Interfero		336	422	46.5	166	8	AD129661	Ad129661	Human
264	428	47.2	166	5	AAAG61815	Aag61815	Interfero		337	422	46.5	166	8	AD129644	Ad129644	Human
265	428	47.2	166	5	AAAM50694	Aam50694	Human	mat	338	422	46.5	166	8	AD129638	Ad129638	Human
266	428	47.2	166	5	ABG68055	Abg68055	Rhesus	in	339	422	46.5	166	8	ADO32430	Ado32430	Human
267	428	47.2	166	6	AAAG79717	Aag79717	Human	IFN	340	422	46.5	189	2	AAAR64240	Aar64240	Human
268	428	47.2	166	7	ADFF70841	Adf70841	Human	alp	341	422	46.5	189	2	AAAM62452	Aam62452	Human
269	428	47.2	166	8	AD128137	Ad128137	Human	int	342	422	46.5	189	2	AAAM94083	Aam94083	Human
270	428	47.2	166	8	AD128628	Ad128628	Human	int	343	422	46.5	189	3	AAAY59395	Aay59395	Human
271	428	47.2	166	8	AD129643	Ad129643	Human	int	344	422	46.5	189	4	AAAE14364	Aae14364	Human
272	428	47.2	166	8	ADL92171	Adl92171	Interfero		345	422	46.5	189	5	ABG68075	Abg68075	Human
273	428	47.2	166	8	ADL88852	Adl88852	Human	cyt	346	422	46.5	189	5	ABG68059	Abg68059	Human
274	428	47.2	166	8	ADM79184	Adm79184	Matucre	hu	347	422	46.5	189	8	ADG32291	Adg32291	Human
275	428	47.2	166	8	ADO32374	Ado32374	Human	int	348	421	46.4	166	4	AAAB94168	Aab94168	Human
276	428	47.2	167	1	AAP20113	Aap20113	Human	int	349	421	46.4	166	4	AAAG61827	Aag61827	Interfero
277	428	47.2	167	1	AAP30185	Aap30185	Sequence		350	421	46.4	166	8	AD129662	Ad129662	Human
278	428	47.2	167	1	AAP80052	Aap80052	Sequence		351	421	46.4	166	8	ADL88860	Adl88860	Human
279	428	47.2	188	1	AAP20013	Aap20013	Hybrid	hu	352	421	46.4	166	8	ADO32353	Ado32353	Human
280	428	47.2	189	1	AAP10020	Aap10020	Sequence		353	421	46.4	166	8	ADO32385	Ado32385	Human
281	428	47.2	189	1	AAP20111	Aap20111	Sequence		354	421	46.4	181	8	ADSS88033	Adss88033	Tunmour
282	428	47.2	189	1	AAP30182	Aap30182	Sequence		355	421	46.4	187	2	AAAG62368	Aag62368	Interfero
283	428	47.2	189	1	AAP40126	Aap40126	Sequence		356	421	46.4	189	5	ABG68066	Abg68066	Human
284	428	47.2	189	2	AAAM53119	Aam53119	Amlno	ac1	357	420	46.3	166	3	AAAY44829	Aay44829	Hybrid
285	428	47.2	189	2	AAAY22636	Aay22636	Human	int	358	420	46.3	166	8	ADO32432	Ado32432	Human
286	428	47.2	189	3	AAAB12967	Aab12967	Human	int	359	420	46.3	188	1	AAP20009	Aap20009	Hybrid
287	428	47.2	189	5	AAE15827	Aae15827	Human	int	360	420	46.3	189	5	ABG68067	Abg68067	Human
288	428	47.2	189	5	ABG68062	Abg68062	Human	int	361	419	46.2	166	3	AAAY44832	Aay44832	Mutanc
289	428	47.2	189	5	ABBO7437	Abb07437	Interfero		362	419	46.2	166	3	AAAY44833	Aay44833	Interfero
290	428	47.2	189	5	AAAG78564	Aag78564	Human	int	363	419	46.2	166	4	AAAG61791	Aag61791	Interfero
291	428	47.2	189	7	ADCT78899	Adct78899	Human	PRO	364	419	46.2	166	4	AAAG61829	Aag61829	Interfero
292	428	47.2	189	7	ABU64301	Abu64301	Human	int	365	419	46.2	166	4	AAAG61806	Aag61806	Interfero
293	428	47.2	189	8	ADN10809	Adn10809	Human	int	366	419	46.2	166	8	AD129639	Ad129639	Human
294	428	47.2	189	8	ADN10809	Adn10809	Human	int	367	419	46.2	166	8	AD129634	Ad129634	Human
295	428	47.2	189	8	ADSL16310	Adsl6310	Human	int	368	419	46.2	166	8	AD129664	Ad129664	Human
296	428	47.2	189	8	ADSL16319	Adsl6319	Human	int	369	419	46.2	166	8	ADO32352	Ado32352	Human
297	427.5	47.1	165	8	ADL88898	Adl88898	Human	cyt	370	419	46.2	188	1	AAP20010	Aap20010	Hybrid
298	426	47.0	166	1	AAP30686	Aap30686	Consensus		371	419	46.2	189	1	AAP20108	Aap20108	Sequence
299	426	47.0	166	5	ABG68079	Abg68079	Human	int	372	419	46.2	189	2	AAAR07680	Aar07680	IFN-alpha
300	426	47.0	167	1	AAAP40180	Aap40180	Sequence		373	419	46.2	189	4	AAAB94780	Aab94780	Human
301	426	47.0	169	1	AAAP40179	Aap40179	Sequence		374	419	46.2	189	5	AAAB42883	Aab42883	Human
302	425	46.9	166	2	AAAR67762	Aar67762	Interfero		375	419	46.2	189	5	ABG68076	Abg68076	Human
303	425	46.9	166	4	AAAG78111	Aag78111	Human	int	376	419	46.2	189	5	ABG68072	Abg68072	Human
304	425	46.9	166	4	AAAG61808	Aag61808	Interfero		377	419	46.2	189	5	ABG68071	Abg68071	Human
305	425	46.9	166	4	AAAG61798	Aag61798	Interfero		378	419	46.2	189	5	ABBO7433	Abb07433	Human
306	425	46.9	166	5	ABG68081	Abg68081	Human	int	379	419	46.2	189	5	AAAG78570	Aag78570	Human
307	425	46.9	166	8	AD129636	Ad129636	Human	int	380	419	46.2	189	7	ABBB98719	Abb98719	Human
308	425	46.9	166	8	AD129626	Ad129626	Human	int	381	419	46.2	189	6	ADPF94972	Adf94972	Human
309	425	46.9	166	8	ADL88855	Adl88855	Human	cyt	382	419	46.2	189	8	ADN10813	Adn10813	Human
310	425	46.9	167	2	AAAR07681	Aar07681	IFN-alpha		383	419	46.2	189	8	ADSL16323	Adsl6323	Human
311	425	46.9	189	1	AAAP30101	Aap30101	Sequence		384	418	46.1	166	4	AAAG61807	Aag61807	Interfero
312	425	46.9	189	1	AAAP50306	Aap50306	Human	int	385	418	46.1	166	8	AD129635	Ad129635	Human
313	425	46.9	189	1	AAAW70373	Aaw70373	Human	int	386	417	46.0	165	1	AAAP30687	Aap30687	IFN-gamma
314	425	46.9	189	5	ABG68068	Abg68068	Human	int	387	417	46.0	166	8	ADO32354	Ado32354	Human
315	425	46.9	189	5	ABG68065	Abg68065	Human	int	388	417	46.0	166	8	ADO32436	Ado32436	Human
316	425	46.9	189	8	ADN10803	Adn10803	Human	int	389	416	45.9	166	4	AAAG61821	Aag61821	Interfero
317	425	46.9	189	8	ADSL16313	Adsl6313	Human	int	390	416	45.9	166	5	ABG68080	Abg68080	Human

391	416	45.9	166	8	AD129649	Ad129649 Human int	464	408	45.0	167	1	AAp60320	AAp60320 Sequence
392	416	45.9	166	8	AD032355	AD032355 Human int	465	408	45.0	164	1	AAp60399	AAp60399 Equine IF
393	416	45.9	166	8	AD032433	AD032433 Human IFN	466	407.5	44.9	162	1	AAp50168	AAp50168 Sequence
394	416	45.9	166	8	AD032442	AD032442 Human IFN	467	407.5	44.9	165	7	ADP16224	ADP16224 Human alb
395	416	45.9	167	1	AAp30184	AAp30184 Sequence	468	407.5	44.9	165	7	ADP16244	ADP16244 Human alb
396	416	45.9	167	1	AAp40128	AAp40128 Sequence	469	407.5	44.9	165	7	ADH21660	ADH21660 Human IFN
397	416	45.9	171	7	ADP30369	ADP30369 Recombina	470	407.5	44.9	165	7	ADH21680	ADH21680 Human IFN
398	416	45.9	169	1	AAp30179	AAp30179 Sequence	471	407.5	44.9	396	8	ADP49583	ADP49583 Human IGG
399	416	45.9	189	1	AAp30164	AAp30164 Sequence	472	407.5	44.9	774	7	ADP16222	ADP16222 Human alb
400	416	45.9	189	1	AAp40123	AAp40123 Sequence	473	407.5	44.9	774	7	ADH21658	ADH21658 Human alb
401	415	45.8	166	3	AAy44974	AAy44974 Human hyb	474	407	44.9	166	3	AApB07338	AApB07338 Mature hu
402	415	45.8	166	3	AAy44826	AAy44826 Hybrid in	475	407	44.9	166	8	AD032346	AD032346 Human int
403	415	45.8	166	4	AAg61813	AAg61813 Interfero	476	407	44.9	166	8	AD032441	AD032441 Human IFN
404	415	45.8	166	5	ABg68056	ABg68056 Rhesus in	477	407	44.9	166	8	AD032393	AD032393 Human IFN
405	415	45.8	166	5	ABg68082	ABg68082 Human int	478	407	44.9	167	1	AAp60317	AAp60317 Sequence
406	415	45.8	166	5	ABg68057	ABg68057 Rhesus in	479	407	44.9	167	8	AD032388	AD032388 Human IFN
407	415	45.8	166	8	AD129641	AD129641 Human int	480	406.5	44.8	168	1	AAp60318	AAp60318 Sequence
408	415	45.8	166	8	AD032444	AD032444 Human IFN	481	406.5	44.8	774	7	ADP16242	ADP16242 Human alb
409	415	45.8	166	8	AD032350	AD032350 Human IFN	482	406.5	44.8	162	5	ABg61678	ABg61678 Human alb
410	414.5	45.7	165	2	AAy43492	AAy43492 A human i	483	406	44.8	162	5	ABg68845	ABg68845 Interfero
411	414.5	45.7	165	2	AAy82887	AAy82887 N-termina	484	406	44.8	166	1	AAp90189	AAp90189 Hybrid al
412	414.5	45.7	166	2	AAy43491	AAy43491 A human i	485	406	44.8	166	3	AApB07344	AApB07344 Mutant hu
413	414.5	45.7	166	2	AAy82805	AAy82805 N-termina	486	406	44.8	166	3	AApB07350	AApB07350 Mature mu
414	414.5	45.7	166	3	AAy82886	AAy82886 Interfero	487	406	44.8	166	5	ABg68839	ABg68839 Interfero
415	414.5	45.7	167	3	AAy82804	AAy82804 Interfero	488	406	44.8	166	5	AD032397	AD032397 Human IFN
416	414.5	45.7	274	2	AAy02097	AAy02097 A multifu	489	406	44.8	198	6	ABP56433	ABP56433 Interfero
417	414.5	45.7	274	2	AAy02092	AAy02092 A multifu	490	405	44.7	166	1	AAp60104	AAp60104 Sequence
418	414.5	45.7	453	2	AAy02093	AAy02093 A multifu	491	405	44.7	166	1	AAp90190	AAp90190 Hybrid al
419	414.5	45.7	453	2	AAy02099	AAy02099 A multifu	492	405	44.7	166	2	AAp42814	AAp42814 Lymphobla
420	414.5	45.7	470	2	AAy02112	AAy02112 A multifu	493	405	44.7	166	2	AAp47008	AAp47008 Recombina
421	414	45.6	166	8	AD032426	AD032426 Human IFN	494	405	44.7	166	2	AAW05337	AAW05337 Alpha-int
422	414	45.6	166	8	AD032446	AD032446 Human IFN	495	405	44.7	166	3	AApB07341	AApB07341 Mutant hu
423	414	45.6	165	3	AAy43357	AAy43357 Human int	496	405	44.7	166	4	AAp49162	AAp49162 Human int
424	413.5	45.6	165	3	AAy44976	AAy44976 Human hyb	497	405	44.7	166	4	ADL88858	ADL88858 Human cyt
425	413.5	45.6	165	3	AAy44828	AAy44828 Hybrid in	498	405	44.7	166	8	AD032429	AD032429 Human IFN
426	413	45.5	166	5	ABg68054	ABg68054 Synthetic	499	405	44.7	166	8	AD032389	AD032389 Human IFN
427	413	45.5	166	5	ABg68058	ABg68058 Rhesus in	500	405	44.7	166	8	AD032427	AD032427 Human IFN
428	413	45.5	166	5	ABg68058	ABg68058 Rhesus in	501	405	44.7	166	8	AD032379	AD032379 Human int
429	413	45.5	166	8	AD032437	AD032437 Human IFN	502	405	44.7	166	8	AD032345	AD032345 Human int
430	413	45.5	166	8	AD032443	AD032443 Human IFN	503	405	44.7	167	1	AAp60222	AAp60222 Sequence
431	412.5	45.5	165	2	AAp11799	AAp11799 Interfero	504	405	44.7	167	1	AAp60316	AAp60316 Sequence
432	412.5	45.5	165	2	ADP16239	ADP16239 Human alb	505	405	44.7	167	2	AAW05336	AAW05336 Alpha-int
433	412.5	45.5	165	7	ADH21675	ADH21675 Human IFN	506	405	44.7	189	1	AAp20112	AAp20112 Sequence
434	412.5	45.5	774	7	ADP16237	ADP16237 Human alb	507	405	44.7	189	5	ABpB07429	ABpB07429 Interfero
435	412.5	45.5	774	7	ADH21673	ADH21673 Human alb	508	405	44.7	189	5	AAg78569	AAg78569 Human int
436	412.5	45.5	166	1	AAp60101	AAp60101 Sequence	509	405	44.7	189	6	AAp27034	AAp27034 Human int
437	412	45.4	166	1	AAp90187	AAp90187 Hybrid al	510	404.5	44.6	165	3	AAy44977	AAy44977 Human hyb
438	412	45.4	166	8	AD032348	AD032348 Human int	511	404.5	44.6	165	8	ADL80663	ADL80663 Human mut
439	412	45.4	166	8	AD032356	AD032356 Human IFN	512	404.5	44.6	165	8	ADL88833	ADL88833 Human mod
440	412	45.4	166	8	AD032439	AD032439 Human IFN	513	404	44.5	166	3	AAy44983	AAy44983 Human mut
441	412	45.4	167	1	AAp60315	AAp60315 Sequence	514	404	44.5	166	3	AAy44979	AAy44979 Human hyb
442	412	45.4	167	1	AAp60314	AAp60314 Sequence	515	404	44.5	166	3	AAy44982	AAy44982 Human mut
443	412	45.4	189	5	ABg68063	ABg68063 Human int	516	404	44.5	166	3	AApB07346	AApB07346 Mutant hu
444	411	45.3	166	8	AD032431	AD032431 Human IFN	517	404	44.5	166	3	AAy44834	AAy44834 Mutant hu
445	411	45.3	166	8	AD032434	AD032434 Human IFN	518	404	44.5	166	3	AAy44835	AAy44835 Mutant hy
446	411	45.3	167	1	AAp70333	AAp70333 Sequence	519	404	44.5	166	4	AAg61801	AAg61801 Interfero
447	410	45.2	166	1	AAp60103	AAp60103 Sequence	520	404	44.5	166	8	AD129629	AD129629 Human int
448	410	45.2	166	3	AApB07343	AApB07343 Mutant hu	521	404	44.5	189	8	ADN10806	ADN10806 Human int
449	410	45.2	166	4	AAg61820	AAg61820 Interfero	522	404	44.5	189	8	ADN16316	ADN16316 Human int
450	410	45.2	166	8	AD129648	AD129648 Human int	523	403.5	44.5	165	3	AAy44981	AAy44981 Human mut
451	410	45.2	166	8	AD032349	AD032349 Human int	524	403.5	44.5	165	3	AAy44980	AAy44980 Human mut
452	409	45.1	166	8	AD032435	AD032435 Human IFN	525	403	44.4	166	1	AAp60102	AAp60102 Sequence
453	409	45.1	166	8	AD032358	AD032358 Human int	526	403	44.4	166	1	AAp90188	AAp90188 Hybrid al
454	409	45.1	166	8	AD032440	AD032440 Human IFN	527	403	44.4	166	3	AAy44978	AAy44978 Human hyb
455	409	45.1	171	1	AAp60764	AAp60764 Plasmid e	528	403	44.4	166	3	AApB07342	AApB07342 Mutant hu
456	408.5	45.0	165	7	ADP16234	ADP16234 Human alb	529	403	44.4	166	3	AAy44830	AAy44830 Hybrid in
457	408.5	45.0	165	7	ADH21670	ADH21670 Human IFN	530	403	44.4	166	8	AD032428	AD032428 Human IFN
458	408.5	45.0	774	7	ADP16232	ADP16232 Human alb	531	403	44.4	166	8	AD032438	AD032438 Human IFN
459	408.5	45.0	774	7	ADH21668	ADH21668 Human alb	532	403	44.4	184	1	AAp61360	AAp61360 Equine IF
460	408	45.0	166	3	AAy53126	AAy53126 Human int	533	403	44.4	184	1	AAp60397	AAp60397 Equine IF
461	408	45.0	166	3	AAy44975	AAy44975 Human hyb	534	402.5	44.4	165	7	ADP16229	ADP16229 Human alb
462	408	45.0	166	3	AAy44827	AAy44827 Hybrid in	535	402.5	44.4	165	7	ADH21665	ADH21665 Human IFN
463	408	45.0	166	8	AD032347	AD032347 Human IFN	536	402.5	44.4	165	8	ADL90662	ADL90662 Human mut

537	402.5	44.4	165	8	ADL90622	Adl190622	Human	mut	610	398.5	43.9	165	8	ADL98645	Adl189645	Human	mod
538	402.5	44.4	165	8	ADL88792	Adl188792	Human	mod	611	398.5	43.9	165	8	ADL88699	Adl188699	Human	mod
539	402.5	44.4	165	8	ADL88832	Adl188832	Human	mod	612	398.5	43.9	165	8	ADL88747	Adl188747	Human	mod
540	402.5	44.4	396	8	ADL84585	Adl184585	Human	IGG	613	398.5	43.9	165	8	ADL88723	Adl188723	Human	mod
541	402.5	44.4	453	2	AAV02095	AAV02095	A	multifu	614	398.5	43.9	165	8	ADL88775	Adl188775	Human	mod
542	402.5	44.4	774	7	ADL16227	Adl16227	Human	alb	615	398.5	43.9	165	8	ADL88698	Adl188698	Human	mod
543	402.5	44.4	774	7	ADH21663	Adh21663	Human	alb	616	398.5	43.9	165	8	ADL88774	Adl188774	Human	mod
544	402	44.3	166	3	AAH07347	AAh07347	Mutant	hu	617	398.5	43.9	165	8	ADL88969	Adl188969	Human	mod
545	401.5	44.3	165	8	ADL90581	Adl190581	Human	mut	618	398.5	43.9	165	8	ADL88668	Adl188668	Human	mod
546	401.5	44.3	165	8	ADL90606	Adl190606	Human	mut	619	398.5	43.9	165	8	ADL88795	Adl188795	Human	mod
547	401.5	44.3	165	8	ADL90668	Adl190668	Human	mut	620	398.5	43.9	165	8	ADL849617	Adl1849617	Human	int
548	401.5	44.3	165	8	ADL90533	Adl190533	Human	mut	621	398.5	43.9	165	8	ADL849614	Adl1849614	Human	int
549	401.5	44.3	165	8	ADL88703	Adl188703	Human	mod	622	398.5	43.9	396	8	ADL849581	Adl1849581	Human	IGG
550	401.5	44.3	165	8	ADL88751	Adl188751	Human	mod	623	398.5	43.9	396	8	ADL849588	Adl1849588	Human	IGG
551	401.5	44.3	165	8	ADL88838	Adl188838	Human	mod	624	398	43.9	102	2	AAW409282	AAW409282	Human	mat
552	401.5	44.3	165	8	ADL88776	Adl188776	Human	mod	625	398	43.9	102	2	AAW44114	AAW44114	Human	int
553	401.5	44.3	396	8	ADL849586	Adl1849586	Human	IGG	626	398	43.9	164	8	ADL023425	ADL023425	Human	IFN
554	401	44.2	166	3	AAH07345	AAh07345	Mutant	hu	627	398	43.9	166	1	AP440210	AP440210	Leukocyte	i
555	401	44.2	166	3	AAH07349	AAh07349	Mutant	hu	628	398	43.9	166	1	AP450424	AP450424	Novel	int
556	401	44.2	166	8	ADH032398	ADh032398	Human	IFN	629	398	43.9	166	2	AAH20053	AAH20053	Human	IFN
557	401	44.2	166	8	ADH032412	ADh032412	Human	IFN	630	398	43.9	166	4	AAH49166	AAH49166	Human	int
558	400.5	44.2	165	2	AAW43384	AAW43384	Human	int	631	398	43.9	166	8	ADH032383	ADH032383	Human	int
559	400.5	44.2	165	8	ADL90598	Adl190598	Human	mut	632	398	43.9	166	8	ADH032424	ADH032424	Human	IFN
560	400.5	44.2	165	8	ADL90542	Adl190542	Human	mut	633	398	43.9	166	8	ADH032387	ADH032387	Human	IFN
561	400.5	44.2	165	8	ADL90506	Adl190506	Human	mut	634	398	43.9	189	1	AAH50104	AAH50104	Sequence	
562	400.5	44.2	165	8	ADL88712	Adl188712	Human	mod	635	398	43.9	189	5	ABH07435	ABH07435	Interfero	
563	400.5	44.2	165	8	ADL88768	Adl188768	Human	mod	636	398	43.9	189	5	AAH78571	AAH78571	Human	int
564	400.5	44.2	165	8	ADL88676	Adl188676	Human	mod	637	398	43.9	189	8	ADH10811	ADH10811	Human	int
565	400.5	44.2	165	8	ADL88851	Adl188851	Human	cyt	638	398	43.9	189	1	ADH16321	ADH16321	Human	int
566	400.5	44.2	165	8	ADL849615	Adl1849615	Human	int	639	397.5	43.8	165	1	AAH50228	AAH50228	Interfero	
567	400.5	44.2	166	1	AAH70329	AAH70329	Sequence		640	397.5	43.8	165	2	AAH62234	AAH62234	Recombina	
568	400.5	44.2	188	2	AAH20564	AAH20564	O-Glycosy		641	397.5	43.8	165	2	AAH14015	AAH14015	Interfero	
569	400.5	44.2	188	2	AAH20549	AAH20549	Human	IFN	642	397.5	43.8	165	2	AAH43379	AAH43379	Human	int
570	400.5	44.2	188	2	AAH66199	AAH66199	E. coli	ST	643	397.5	43.8	165	2	AAH02090	AAH02090	A	multifu
571	400.5	44.2	396	8	ADL849587	Adl1849587	Human	IGG	644	397.5	43.8	165	2	AAH02091	AAH02091	A	multifu
572	400.5	44.2	396	8	ADL849584	Adl1849584	Human	IGG	645	397.5	43.8	165	2	AAH43488	AAH43488	A	human i
573	400	44.1	166	3	AAH07348	AAh07348	Mutant	hu	646	397.5	43.8	165	2	AAH43489	AAH43489	A	human i
574	400	44.1	166	8	ADH032344	ADh032344	Human	int	647	397.5	43.8	165	2	AAH43490	AAH43490	A	human i
575	400	44.1	433	2	AAH01579	AAH01579	Interfero		648	397.5	43.8	165	3	AAH82884	AAH82884	Interfero	
576	399.5	44.0	165	4	AAH06746	AAH06746	Human	int	649	397.5	43.8	165	3	AAH82885	AAH82885	N-termi	
577	399.5	44.0	165	8	ADL90517	Adl190517	Human	mut	650	397.5	43.8	165	3	AAH82883	AAH82883	Interfero	
578	399.5	44.0	165	8	ADL90565	Adl190565	Human	mut	651	397.5	43.8	165	5	AAH50705	AAH50705	Human	mat
579	399.5	44.0	165	8	ADL90558	Adl190558	Human	mut	652	397.5	43.8	165	5	AAH50693	AAH50693	Human	mat
580	399.5	44.0	165	8	ADL90596	Adl190596	Human	mut	653	397.5	43.8	165	5	AAH18958	AAH18958	Human	int
581	399.5	44.0	165	8	ADL90599	Adl190599	Human	mut	654	397.5	43.8	165	7	ADH8104	ADH8104	Human	int
582	399.5	44.0	165	8	ADL90499	Adl190499	Human	mut	655	397.5	43.8	165	7	ADH15325	ADH15325	Human	alb
583	399.5	44.0	165	8	ADL90502	Adl190502	Human	mut	656	397.5	43.8	165	7	ADH15304	ADH15304	Human	alb
584	399.5	44.0	165	8	ADL88728	Adl188728	Human	mod	657	397.5	43.8	165	7	ADH15270	ADH15270	Human	alb
585	399.5	44.0	165	8	ADL88769	Adl188769	Human	mod	658	397.5	43.8	165	7	ADH16215	ADH16215	Human	alb
586	399.5	44.0	165	8	ADL88735	Adl188735	Human	mod	659	397.5	43.8	165	7	ADH15320	ADH15320	Human	alb
587	399.5	44.0	165	8	ADL88766	Adl188766	Human	mod	660	397.5	43.8	165	7	ADH15321	ADH15321	Human	alb
588	399.5	44.0	165	8	ADL88669	Adl188669	Human	mod	661	397.5	43.8	165	7	ADH15315	ADH15315	Human	alb
589	399.5	44.0	165	8	ADL88687	Adl188687	Human	mod	662	397.5	43.8	165	7	ADH70840	ADH70840	Human	alb
590	399.5	44.0	165	8	ADL88672	Adl188672	Human	mod	663	397.5	43.8	165	7	ADH21397	ADH21397	Human	int
591	399	44.0	184	1	AAH60404	AAH60404	Equine	IF	664	397.5	43.8	165	7	ADH21400	ADH21400	Human	int
592	399	44.0	189	5	AAH81097	AAH81097	Porcine	I	665	397.5	43.8	165	7	ADH21387	ADH21387	Human	int
593	399	44.0	189	6	AAH98720	AAH98720	Human	alp	666	397.5	43.8	165	7	ADH21657	ADH21657	Human	IFN
594	398.5	43.9	165	8	ADL90624	Adl190624	Human	mut	667	397.5	43.8	165	7	ADH21375	ADH21375	Human	int
595	398.5	43.9	165	8	ADL90577	Adl190577	Human	mut	668	397.5	43.8	165	7	ADH21396	ADH21396	Human	int
596	398.5	43.9	165	8	ADL90633	Adl190633	Human	mut	669	397.5	43.8	165	7	ADH21392	ADH21392	Human	int
597	398.5	43.9	165	8	ADL90528	Adl190528	Human	mut	670	397.5	43.8	165	7	ADH20497	ADH20497	Human	int
598	398.5	43.9	165	8	ADL90605	Adl190605	Human	mut	671	397.5	43.8	165	8	ADL90626	ADL90626	Human	mut
599	398.5	43.9	165	8	ADL90529	Adl190529	Human	mut	672	397.5	43.8	165	8	ADL90588	ADL90588	Human	mut
600	398.5	43.9	165	8	ADL90553	Adl190553	Human	mut	673	397.5	43.8	165	8	ADL90568	ADL90568	Human	mut
601	398.5	43.9	165	8	ADL90669	Adl190669	Human	mut	674	397.5	43.8	165	8	ADL90559	ADL90559	Human	mut
602	398.5	43.9	165	8	ADL90498	Adl190498	Human	mut	675	397.5	43.8	165	8	ADL90623	ADL90623	Human	mut
603	398.5	43.9	165	8	ADL90604	Adl190604	Human	mut	676	397.5	43.8	165	8	ADL90670	ADL90670	Human	mut
604	398.5	43.9	165	8	ADL90694	Adl190694	Human	mut	677	397.5	43.8	165	8	ADL90501	ADL90501	Human	mut
605	398.5	43.9	165	8	ADL90692	Adl190692	Human	mut	678	397.5	43.8	165	8	ADL90593	ADL90593	Human	mut
606	398.5	43.9	165	8	ADL90625	Adl190625	Human	mut	679	397.5	43.8	165	8	ADL90511	ADL90511	Human	mut
607	398.5	43.9	165	8	ADL88803	Adl188803	Human	mod	680	397.5	43.8	165	8	ADL90574	ADL90574	Human	mut
608	398.5	43.9	165	8	ADL88839	Adl188839	Human	mod	681	397.5	43.8	165	8	ADL90603	ADL90603	Human	mut
609	398.5	43.9	165	8	ADL88794	Adl188794	Human	mod	682	397.5	43.8	165	8	ADL90503	ADL90503	Human	mut

683	397.5	43.8	165	8	ADL90597	AdI90597	Human	mut	756	396.5	43.7	165	8	ADL90505	AdI90505	Human	mut
684	397.5	43.8	165	8	ADL90620	AdI90620	Human	mut	757	396.5	43.7	165	8	ADL90557	AdI90557	Human	mut
685	397.5	43.8	165	8	ADL90612	AdI90612	Human	mut	758	396.5	43.7	165	8	ADL90575	AdI90575	Human	mut
686	397.5	43.8	165	8	ADL90602	AdI90602	Human	mut	759	396.5	43.7	165	8	ADL90615	AdI90615	Human	mut
687	397.5	43.8	165	8	ADL88763	AdI88763	Human	mod	760	396.5	43.7	165	8	ADL90671	AdI90671	Human	mut
688	397.5	43.8	165	8	ADL88729	AdI88729	Human	mod	761	396.5	43.7	165	8	ADL90672	AdI90672	Human	mut
689	397.5	43.8	165	8	ADL88681	AdI88681	Human	mod	762	396.5	43.7	165	8	ADL90508	AdI90508	Human	mut
690	397.5	43.8	165	8	ADL88667	AdI88667	Human	cyt	763	396.5	43.7	165	8	ADL90549	AdI90549	Human	mut
691	397.5	43.8	165	8	ADL88790	AdI88790	Human	mod	764	396.5	43.7	165	8	ADL90589	AdI90589	Human	mut
692	397.5	43.8	165	8	ADL88837	AdI88837	Human	mod	765	396.5	43.7	165	8	ADL90702	AdI90702	Human	mut
693	397.5	43.8	165	8	ADL88782	AdI88782	Human	mod	766	396.5	43.7	165	8	ADL90627	AdI90627	Human	mut
694	397.5	43.8	165	8	ADL88758	AdI88758	Human	mod	767	396.5	43.7	165	8	ADL90531	AdI90531	Human	mut
695	397.5	43.8	165	8	ADL88793	AdI88793	Human	mod	768	396.5	43.7	165	8	ADL90655	AdI90655	Human	mut
696	397.5	43.8	165	8	ADL88840	AdI88840	Human	mod	769	396.5	43.7	165	8	ADL90700	AdI90700	Human	mut
697	397.5	43.8	165	8	ADL88673	AdI88673	Human	mod	770	396.5	43.7	165	8	ADL90563	AdI90563	Human	mut
698	397.5	43.8	165	8	ADL88738	AdI88738	Human	mod	771	396.5	43.7	165	8	ADL90595	AdI90595	Human	mut
699	397.5	43.8	165	8	ADL88772	AdI88772	Human	mod	772	396.5	43.7	165	8	ADL90664	AdI90664	Human	mut
700	397.5	43.8	165	8	ADL88744	AdI88744	Human	mod	773	396.5	43.7	165	8	ADL90678	AdI88678	Human	mod
701	397.5	43.8	165	8	ADL88767	AdI88767	Human	mod	774	396.5	43.7	165	8	ADL88825	AdI88825	Human	mod
702	397.5	43.8	165	8	ADL88796	AdI88796	Human	mod	775	396.5	43.7	165	8	ADL88834	AdI88834	Human	mod
703	397.5	43.8	165	8	ADL88773	AdI88773	Human	mod	776	396.5	43.7	165	8	ADL88675	AdI88675	Human	mod
704	397.5	43.8	165	8	ADL88671	AdI88671	Human	mod	777	396.5	43.7	165	8	ADL88785	AdI88785	Human	mod
705	397.5	43.8	165	8	AD032375	Ad032375	Human	int	778	396.5	43.7	165	8	ADL88797	AdI88797	Human	mod
706	397.5	43.8	165	8	ADSI17969	AdSI17969	Transgeni		779	396.5	43.7	165	8	ADL88842	AdI88842	Human	mod
707	397.5	43.8	165	8	ADRA49576	Adr49576	Human	int	780	396.5	43.7	165	8	ADL88733	AdI88733	Human	mod
708	397.5	43.8	166	1	AAPE20114	AAp20114	Human	int	781	396.5	43.7	165	8	ADL88701	AdI88701	Human	mod
709	397.5	43.8	166	2	AAW05039	AAw05039	Sequence		782	396.5	43.7	165	8	ADL88745	AdI88745	Human	mod
710	397.5	43.8	166	2	AAW05040	AAw05040	Protein #		783	396.5	43.7	165	8	ADL88841	AdI88841	Human	mod
711	397.5	43.8	166	3	AAW82803	AAy82803	N-termi		784	396.5	43.7	165	8	ADL89653	AdI89653	Human	mod
712	397.5	43.8	166	4	AAAG5241	AAg5241	Human	alp	785	396.5	43.7	165	8	ADL88719	AdI88719	Human	mod
713	397.5	43.8	166	5	AAU98666	AAu98666	Human	int	786	396.5	43.7	165	8	ADL88765	AdI88765	Human	mod
714	397.5	43.8	166	8	ADN10802	Adn10802	Human	int	787	396.5	43.7	165	8	ADL89651	AdI89651	Human	mod
715	397.5	43.8	166	8	AD081955	Adq81955	Human	int	788	396.5	43.7	165	8	ADL88727	AdI88727	Human	mod
716	397.5	43.8	166	8	ADSI6312	AdSI6312	Human	int	789	396.5	43.7	165	8	AD032409	Ad032409	Human	mod
717	397.5	43.8	167	3	AAy82802	AAy82802	Interfero		790	396	43.7	164	8	AD032396	Ad032396	Human	IFN
718	397.5	43.8	167	3	AAE16138	AAE16138	Human	IFN	791	396	43.7	166	8	AAW43382	AAw43382	Human	int
719	397.5	43.8	182	1	AAy42486	AAy42486	Human	int	792	396.5	43.6	165	8	ADL90580	AdI90580	Human	mut
720	397.5	43.8	182	2	AAy02094	AAy02094	A multi-fu		793	395.5	43.6	165	8	ADL90534	AdI90534	Human	mut
721	397.5	43.8	188	5	AAE15828	AAE15828	Human	int	794	395.5	43.6	165	8	ADL90576	AdI90576	Human	mut
722	397.5	43.8	188	5	AAE15957	AAE15957	Human	alp	795	395.5	43.6	165	8	ADL90591	AdI90591	Human	mut
723	397.5	43.8	188	5	ABB07434	ABb07434	Interfero		796	395.5	43.6	165	8	ADL90521	AdI90521	Human	mut
724	397.5	43.8	188	6	ABRS5840	ABr55840	Human	int	797	395.5	43.6	165	8	ADL90579	AdI90579	Human	mut
725	397.5	43.8	188	6	AAO16454	AAo16454	Human	int	798	395.5	43.6	165	8	ADL90621	AdI90621	Human	mut
726	397.5	43.8	188	8	ADP77247	AdP77247	Interfero		799	395.5	43.6	165	8	ADL90634	AdI90634	Human	mut
727	397.5	43.8	188	8	ADL24486	AdL24486	Human	int	800	395.5	43.6	165	8	ADL90665	AdI90665	Human	mut
728	397.5	43.8	188	8	ADN49676	Adn49676	Human	int	801	395.5	43.6	165	8	ADL90654	AdI90654	Human	mut
729	397.5	43.8	188	8	AAE16138	AAE16138	Human	IFN	802	395.5	43.6	165	8	ADL90500	AdI90500	Human	mut
730	397.5	43.8	198	5	AAE16138	AAE16138	Human	IFN	803	395.5	43.6	165	8	ADL90607	AdI90607	Human	mut
731	397.5	43.8	274	2	AAy02098	AAy02098	A multi-fu		804	395.5	43.6	165	8	ADL90534	AdI90534	Human	mut
732	397.5	43.8	274	2	AAy02098	AAy02098	A multi-fu		805	395.5	43.6	165	8	ADL90587	AdI90587	Human	mut
733	397.5	43.8	274	4	AAAB72223	AAb72223	Fusion pr		806	395.5	43.6	165	8	ADL90509	AdI90509	Human	mut
734	397.5	43.8	396	6	ADRA49580	Adr49580	Human	Igg	807	395.5	43.6	165	8	ADL90513	AdI90513	Human	mut
735	397.5	43.8	411	8	ADRA49602	Adr49602	Human	Igg	808	395.5	43.6	165	8	ADL90556	AdI90556	Human	mut
736	397.5	43.8	453	2	AAy02096	AAy02096	A multi-fu		809	395.5	43.6	165	8	ADL90578	AdI90578	Human	mut
737	397.5	43.8	769	7	ADFI5090	AdFI5090	Human	alb	810	395.5	43.6	165	8	ADL90590	AdI90590	Human	mut
738	397.5	43.8	769	7	ADFI5111	AdFI5111	Human	alb	811	395.5	43.6	165	8	ADL88761	AdI88761	Human	mod
739	397.5	43.8	769	7	ADH21331	Adh21331	Human	alb	812	395.5	43.6	165	8	ADL88704	AdI88704	Human	mod
740	397.5	43.8	769	7	ADH21318	Adh21318	Human	alb	813	395.5	43.6	165	8	ADL88679	AdI88679	Human	mod
741	397.5	43.8	773	7	ADFI5107	AdFI5107	Human	alb	814	395.5	43.6	165	8	ADL88746	AdI88746	Human	mod
742	397.5	43.8	773	7	ADH21328	Adh21328	Human	alb	815	395.5	43.6	165	8	ADL88757	AdI88757	Human	mod
743	397.5	43.8	774	7	ADFI5106	AdFI5106	Human	alb	816	395.5	43.6	165	8	ADL88824	AdI88824	Human	mod
744	397.5	43.8	774	7	ADFI5106	AdFI5106	Human	alb	817	395.5	43.6	165	8	ADL88778	AdI88778	Human	mod
745	397.5	43.8	774	7	ADFI5106	AdFI5106	Human	alb	818	395.5	43.6	165	8	ADL88777	AdI88777	Human	mod
746	397.5	43.8	774	7	ADFI5056	AdFI5056	Human	alb	819	395.5	43.6	165	8	ADL88683	AdI88683	Human	mod
747	397.5	43.8	774	7	ADH21306	Adh21306	Human	alb	820	395.5	43.6	165	8	ADL88726	AdI88726	Human	mod
748	397.5	43.8	774	7	ADH21655	Adh21655	Human	alb	821	395.5	43.6	165	8	ADL88750	AdI88750	Human	mod
749	397.5	43.8	835	7	ADH21327	Adh21327	Human	alb	822	395.5	43.6	165	8	ADL88749	AdI88749	Human	mod
750	397.5	43.8	835	7	ADFI5101	AdFI5101	Human	alb	823	395.5	43.6	165	8	ADL88750	AdI88750	Human	mod
751	397.5	43.8	835	7	ADH21323	Adh21323	Human	alb	824	395.5	43.6	165	8	ADL88691	AdI88691	Human	mod
752	396.5	43.7	165	1	AAPE60221	AAp60221	Sequence		825	395.5	43.6	165	8	ADL88748	AdI88748	Human	mod
753	396.5	43.7	165	1	AAPE70327	AAp70327	Recondina		826	395.5	43.6	165	8	ADL88835	AdI88835	Human	mod
754	396.5	43.7	165	4	AAW43385	AAw43385	Human	int	827	395.5	43.6	165	8				
755	396.5	43.7	165	4	AAE06745	AAe06745	Human	int	828	395.5	43.6	165	8				

829	395.5	43.6	165	8	ADL88670	Adl88670	Human	mod	902	393.5	43.4	165	8	ADL90651	Adl90651	Human	mut
830	395.5	43.6	165	8	ADL88791	Adl88791	Human	mod	903	393.5	43.4	165	8	ADL90600	Adl90600	Human	mut
831	395.5	43.6	165	8	ADL88804	Adl88804	Human	mod	904	393.5	43.4	165	8	ADL90695	Adl90695	Human	mut
832	395.5	43.6	166	8	ADL90395	Adl90395	Human	IFN	905	393.5	43.4	165	8	ADL90698	Adl90698	Human	mut
833	395.5	43.6	216	2	AAAR3793	Aear3793	Natural	h	906	393.5	43.4	165	8	ADL90617	Adl90617	Human	mut
834	394.5	43.5	165	2	AAW43387	Aaw43387	Human	int	907	393.5	43.4	165	8	ADL90650	Adl90650	Human	mut
835	394.5	43.5	165	3	AAAB01301	Aab01301	Wild type		908	393.5	43.4	165	8	ADL90677	Adl90677	Human	mut
836	394.5	43.5	165	4	AAAB4158	Aab4158	Human	int	909	393.5	43.4	165	8	ADL90649	Adl90649	Human	mut
837	394.5	43.5	165	8	ADL90516	Adl90516	Human	mut	910	393.5	43.4	165	8	ADL90538	Adl90538	Human	mut
838	394.5	43.5	165	8	ADL90555	Adl90555	Human	mut	911	393.5	43.4	165	8	ADL90610	Adl90610	Human	mut
839	394.5	43.5	165	8	ADL90518	Adl90518	Human	mut	912	393.5	43.4	165	8	ADL90616	Adl90616	Human	mut
840	394.5	43.5	165	8	ADL90594	Adl90594	Human	mut	913	393.5	43.4	165	8	ADL90619	Adl90619	Human	mut
841	394.5	43.5	165	8	ADL90630	Adl90630	Human	mut	914	393.5	43.4	165	8	ADL90648	Adl90648	Human	mut
842	394.5	43.5	165	8	ADL90585	Adl90585	Human	mut	915	393.5	43.4	165	8	ADL90632	Adl90632	Human	mut
843	394.5	43.5	165	8	ADL90541	Adl90541	Human	mut	916	393.5	43.4	165	8	ADL90536	Adl90536	Human	mut
844	394.5	43.5	165	8	ADL90532	Adl90532	Human	mut	917	393.5	43.4	165	8	ADL90676	Adl90676	Human	mut
845	394.5	43.5	165	8	ADL90592	Adl90592	Human	mut	918	393.5	43.4	165	8	ADL89646	Adl89646	Human	mod
846	394.5	43.5	165	8	ADL90530	Adl90530	Human	mut	919	393.5	43.4	165	8	ADL88770	Adl88770	Human	mod
847	394.5	43.5	165	8	ADL90572	Adl90572	Human	mut	920	393.5	43.4	165	8	ADL88787	Adl88787	Human	mod
848	394.5	43.5	165	8	ADL90631	Adl90631	Human	mut	921	393.5	43.4	165	8	ADL88780	Adl88780	Human	mod
849	394.5	43.5	165	8	ADL90608	Adl90608	Human	mut	922	393.5	43.4	165	8	ADL88820	Adl88820	Human	mod
850	394.5	43.5	165	8	ADL90515	Adl90515	Human	mut	923	393.5	43.4	165	8	ADL88821	Adl88821	Human	mod
851	394.5	43.5	165	8	ADL90583	Adl90583	Human	mut	924	393.5	43.4	165	8	ADL88802	Adl88802	Human	mod
852	394.5	43.5	165	8	ADL90550	Adl90550	Human	mut	925	393.5	43.4	165	8	ADL88785	Adl88785	Human	mod
853	394.5	43.5	165	8	ADL90562	Adl90562	Human	mut	926	393.5	43.4	165	8	ADL88789	Adl88789	Human	mod
854	394.5	43.5	165	8	ADL88778	Adl88778	Human	mod	927	393.5	43.4	165	8	ADL88819	Adl88819	Human	mod
855	394.5	43.5	165	8	ADL88702	Adl88702	Human	mod	928	393.5	43.4	165	8	ADL89649	Adl89649	Human	mod
856	394.5	43.5	165	8	ADL88848	Adl88848	Human	cyt	929	393.5	43.4	165	8	ADL88818	Adl88818	Human	mod
857	394.5	43.5	165	8	ADL88725	Adl88725	Human	mod	930	393.5	43.4	165	8	ADL88847	Adl88847	Human	mod
858	394.5	43.5	165	8	ADL88742	Adl88742	Human	mod	931	393.5	43.4	165	8	ADL88708	Adl88708	Human	mod
859	394.5	43.5	165	8	ADL88764	Adl88764	Human	mod	932	393.5	43.4	165	8	ADL88706	Adl88706	Human	mod
860	394.5	43.5	165	8	ADL89773	Adl89773	Human	cyt	933	393.5	43.4	165	8	ADL88846	Adl88846	Human	mod
861	394.5	43.5	165	8	ADL88688	Adl88688	Human	mod	934	393.5	43.4	187	1	AAAP20007	Aap20007	Hybrid	hu
862	394.5	43.5	165	8	ADL88720	Adl88720	Human	mod	935	393	43.3	160	8	ADL90504	Adl90504	Human	IFN
863	394.5	43.5	165	8	ADL88801	Adl88801	Human	mod	936	393	43.3	166	1	AAAP60099	Aap60099	Sequence	
864	394.5	43.5	165	8	ADL88762	Adl88762	Human	mod	937	393	43.3	166	1	AAAP90185	Aap90185	Hybrid	al
865	394.5	43.5	165	8	ADL88800	Adl88800	Human	mod	938	393	43.3	165	8	ADL90512	Adl90512	Human	mut
866	394.5	43.5	165	8	ADL88700	Adl88700	Human	mod	939	392.5	43.3	165	8	ADL90545	Adl90545	Human	mut
867	394.5	43.5	165	8	ADL88711	Adl88711	Human	mod	940	392.5	43.3	165	8	ADL90609	Adl90609	Human	int
868	394.5	43.5	165	8	ADL88686	Adl88686	Human	mod	941	392.5	43.3	165	8	ADL90613	Adl90613	Human	mut
869	394.5	43.5	165	8	ADL88685	Adl88685	Human	mod	942	392.5	43.3	165	8	ADL90573	Adl90573	Human	mut
870	394.5	43.5	165	8	ADL88753	Adl88753	Human	mod	943	392.5	43.3	165	8	ADL90675	Adl90675	Human	mut
871	394.5	43.5	165	8	ADL88755	Adl88755	Human	mod	944	392.5	43.3	165	8	ADL90547	Adl90547	Human	mut
872	394.5	43.5	165	8	ADL88732	Adl88732	Human	mod	945	392.5	43.3	165	8	ADL90554	Adl90554	Human	mut
873	394.5	43.5	165	8	ADN10801	Adn10801	Human	int	946	392.5	43.3	165	8	ADL90696	Adl90696	Human	mut
874	394.5	43.5	165	8	ADSL16311	Adsl16311	Human	int	947	392.5	43.3	165	8	ADL90504	Adl90504	Human	mut
875	394.5	43.5	166	1	AAAP40022	Aap40022	Recombina		948	392.5	43.3	165	8	ADL90510	Adl90510	Human	mut
876	394.5	43.5	166	4	AAAB82337	Aab82337	Yeast-exp		949	392.5	43.3	165	8	ADL90512	Adl90512	Human	mut
877	394.5	43.5	175	1	AAAP30163	Aap30163	Sequence		950	392.5	43.3	165	8	ADL90586	Adl90586	Human	mut
878	394.5	43.5	182	2	AAAR05400	Aar05400	Hybrid	hu	951	392.5	43.3	165	8	ADL90545	Adl90545	Human	mut
879	394.5	43.5	188	1	AAAP20103	Aap20103	Sequence		952	392.5	43.3	165	8	ADL90582	Adl90582	Human	mut
880	394.5	43.5	188	4	AAAB31458	Aab31458	Amino aci		953	392.5	43.3	165	8	ADL90584	Adl90584	Human	mut
881	394.5	43.5	188	5	AAAE15826	Aae15826	Human	int	954	392.5	43.3	165	8	ADL90537	Adl90537	Human	mut
882	394.5	43.5	188	5	AAAB80767	Aab80767	Human	int	955	392.5	43.3	165	8	ADL90618	Adl90618	Human	mut
883	394.5	43.5	188	8	ADPF7281	Adf7281	Interfero		956	392.5	43.3	165	8	ADL90520	Adl90520	Human	mut
884	394.5	43.5	188	8	ADU99992	Adu99992	Human	IFN	957	392.5	43.3	165	8	ADL90567	Adl90567	Human	mut
885	394.5	43.5	188	8	ADMA41331	Adm41331	Human	int	958	392.5	43.3	165	8	ADL88743	Adl88743	Human	mod
886	394.5	43.5	188	8	ADN02798	Adn02798	Human	int	959	392.5	43.3	165	8	ADL88783	Adl88783	Human	mod
887	394.5	43.5	188	4	AAAB82338	Aab82338	Human	int	960	392.5	43.3	165	8	ADL88682	Adl88682	Human	mod
888	394.5	43.5	344	5	AAAB06343	Aab06343	Human	int	961	392.5	43.3	165	8	ADL88737	Adl88737	Human	mod
889	394	43.4	166	4	AAAG61809	Aag61809	Interfero		962	392.5	43.3	165	8	ADL88674	Adl88674	Human	mod
890	394	43.4	166	8	ADL29637	Adl29637	Human	int	963	392.5	43.3	165	8	ADL88717	Adl88717	Human	mod
891	394	43.4	166	8	ADL90390	Adl90390	Human	IFN	964	392.5	43.3	165	8	ADL89647	Adl89647	Human	mod
892	394	43.4	166	8	ADL903404	Adl903404	Human	IFN	965	392.5	43.3	165	8	ADL88707	Adl88707	Human	mod
893	394	43.4	166	8	ADL903413	Adl903413	Human	IFN	966	392.5	43.3	165	8	ADL88754	Adl88754	Human	mod
894	394	43.4	166	8	ADL903420	Adl903420	Human	IFN	967	392.5	43.3	165	8	ADL88756	Adl88756	Human	mod
895	394	43.4	166	8	ADL9032416	Adl9032416	Human	IFN	968	392.5	43.3	165	8	ADL88845	Adl88845	Human	mod
896	394	43.4	166	8	ADL903419	Adl903419	Human	IFN	969	392.5	43.3	165	8	ADL88690	Adl88690	Human	mod
897	394	43.4	166	8	ADL903422	Adl903422	Human	IFN	970	392.5	43.3	165	8	ADL88779	Adl88779	Human	mod
898	394	43.4	166	8	ADL9032392	Adl9032392	Human	IFN	971	392.5	43.3	165	8	ADL88788	Adl88788	Human	mod
899	394	43.4	189	5	AAAG68064	Aag68064	Human	int	972	392.5	43.3	165	8	ADL88752	Adl88752	Human	mod
900	393.5	43.4	165	2	AAW43383	Aaw43383	Human	int	973	392.5	43.3	165	8	ADL88680	Adl88680	Human	mod
901	393.5	43.4	165	7	ADL13053	Adl13053	Modified		974	392.5	43.3	165	8	ADL88715	Adl88715	Human	mod

975	392.5	43.3	165	8	ADL88724	ADL88724	Human	mod	1048	389.5	42.9	165	8	ADL90629	ADL90629	Human	mut
976	392	43.2	166	4	AA61822	AA61822	Interfero		1049	389.5	42.9	165	8	ADL90544	ADL90544	Human	mut
977	392	43.2	166	8	AD129650	AD129650	Human	int	1050	389.5	42.9	165	8	ADL90639	ADL90639	Human	mut
978	392	43.2	166	8	AD032399	AD032399	Human	IFN	1051	389.5	42.9	165	8	ADL90522	ADL90522	Human	mut
979	392	43.2	166	8	AD032391	AD032391	Human	IFN	1052	389.5	42.9	165	8	ADL90543	ADL90543	Human	mut
980	392	43.2	189	4	AA849782	AA849782	Human	alp	1053	389.5	42.9	165	8	ADL90552	ADL90552	Human	mut
981	392	43.2	189	7	ADF94974	ADF94974	Human	int	1054	389.5	42.9	165	8	ADL88814	ADL88814	Human	mod
982	391.5	43.2	189	2	AAW43390	AAW43390	Human	int	1055	389.5	42.9	165	8	ADL88784	ADL88784	Human	mod
983	391.5	43.2	165	2	AAW43386	AAW43386	Human	int	1056	389.5	42.9	165	8	ADL88713	ADL88713	Human	mod
984	391.5	43.2	165	7	AD113046	AD113046	Wild-cypr		1057	389.5	42.9	165	8	ADL88652	ADL88652	Human	mod
985	391.5	43.2	165	8	AD125136	AD125136	Human	int	1058	389.5	42.9	165	8	ADL88694	ADL88694	Human	mod
986	391.5	43.2	165	8	ADL90561	ADL90561	Human	mut	1059	389.5	42.9	165	8	ADL88828	ADL88828	Human	mod
987	391.5	43.2	165	8	ADL90560	ADL90560	Human	mut	1060	389.5	42.9	165	8	ADL88716	ADL88716	Human	mod
988	391.5	43.2	165	8	ADL90611	ADL90611	Human	mut	1061	389.5	42.9	165	8	ADL88722	ADL88722	Human	mod
989	391.5	43.2	165	8	ADL90703	ADL90703	Human	mut	1062	389.5	42.9	165	8	ADL88739	ADL88739	Human	mod
990	391.5	43.2	165	8	ADL90566	ADL90566	Human	mut	1063	389.5	42.9	165	8	ADL89650	ADL89650	Human	mod
991	391.5	43.2	165	8	ADL90571	ADL90571	Human	mut	1064	389.5	42.9	165	8	ADL88696	ADL88696	Human	mod
992	391.5	43.2	165	8	ADL90667	ADL90667	Human	mut	1065	389.5	42.9	165	8	ADL88843	ADL88843	Human	mod
993	391.5	43.2	165	8	ADL90701	ADL90701	Human	mut	1066	389.5	42.9	165	8	ADL88716	ADL88716	Human	mod
994	391.5	43.2	165	8	ADL90525	ADL90525	Human	mut	1067	389.5	42.9	165	8	ADL88705	ADL88705	Human	mod
995	391.5	43.2	165	8	ADL90693	ADL90693	Human	mut	1068	389.5	42.9	166	1	AA640759	AA640759	Human	int
996	391.5	43.2	165	8	ADL90540	ADL90540	Human	mut	1069	389.5	42.9	430	4	AA655234	AA655234	Human	leu
997	391.5	43.2	165	8	ADL90507	ADL90507	Human	mut	1070	389.5	42.9	166	8	AD032402	AD032402	Human	IFN
998	391.5	43.2	165	8	ADL90527	ADL90527	Human	mut	1071	388.5	42.8	165	8	ADL90645	ADL90645	Human	mut
999	391.5	43.2	165	8	ADL90539	ADL90539	Human	mut	1072	388.5	42.8	165	8	ADL90674	ADL90674	Human	mut
1000	391.5	43.2	165	8	ADL90666	ADL90666	Human	mut	1073	388.5	42.8	165	8	ADL90659	ADL90659	Human	mut
1001	391.5	43.2	165	8	ADL90601	ADL90601	Human	mut	1074	388.5	42.8	165	8	ADL90519	ADL90519	Human	mut
1002	391.5	43.2	165	8	ADL90514	ADL90514	Human	mut	1075	388.5	42.8	165	8	ADL90564	ADL90564	Human	mut
1003	391.5	43.2	165	8	ADL90523	ADL90523	Human	mut	1076	388.5	42.8	165	8	ADL90569	ADL90569	Human	mut
1004	391.5	43.2	165	8	ADL88695	ADL88695	Human	mod	1077	388.5	42.8	165	8	ADL88689	ADL88689	Human	mod
1005	391.5	43.2	165	8	ADL88836	ADL88836	Human	mod	1078	388.5	42.8	165	8	ADL88844	ADL88844	Human	mod
1006	391.5	43.2	165	8	ADL88741	ADL88741	Human	mod	1079	388.5	42.8	165	8	ADL88829	ADL88829	Human	mod
1007	391.5	43.2	165	8	ADL88693	ADL88693	Human	mod	1080	388.5	42.8	165	8	ADL88734	ADL88734	Human	mod
1008	391.5	43.2	165	8	ADL89644	ADL89644	Human	mod	1081	388.5	42.8	165	8	ADL88815	ADL88815	Human	mod
1009	391.5	43.2	165	8	ADL88731	ADL88731	Human	mod	1082	388.5	42.8	165	8	ADL88739	ADL88739	Human	mod
1010	391.5	43.2	165	8	ADL88709	ADL88709	Human	mod	1083	388.5	42.8	165	8	ADL94612	ADL94612	Human	int
1011	391.5	43.2	165	8	ADL89652	ADL89652	Human	mod	1084	388.5	42.8	366	8	ADL94950	ADL94950	Human	igg
1012	391.5	43.2	165	8	ADL88697	ADL88697	Human	mod	1085	388.5	42.8	189	6	AA015998	AA015998	Mutant	hu
1013	391.5	43.2	165	8	ADL88736	ADL88736	Human	mod	1086	388.5	42.7	165	8	ADL90656	ADL90656	Human	mut
1014	391.5	43.2	165	8	ADL88730	ADL88730	Human	mod	1087	387.5	42.7	165	8	ADL90642	ADL90642	Human	mut
1015	391.5	43.2	165	8	ADL88781	ADL88781	Human	mod	1088	387.5	42.7	165	8	ADL88826	ADL88826	Human	mod
1016	391.5	43.2	165	8	ADL89654	ADL89654	Human	mod	1089	387.5	42.7	165	8	ADL88812	ADL88812	Human	mod
1017	391.5	43.2	165	8	ADL88684	ADL88684	Human	mod	1090	387.5	42.7	164	1	AA660119	AA660119	Interfero	
1018	391.5	43.2	165	8	ADL88710	ADL88710	Human	mod	1091	387.5	42.7	167	3	AA651930	AA651930	Human	alp
1019	391.5	43.2	165	8	ADL88771	ADL88771	Human	mod	1092	387	42.7	165	5	AB668843	AB668843	Interfero	
1020	391.5	43.2	165	8	ADL88677	ADL88677	Human	mod	1093	386.5	42.6	165	7	AD113054	AD113054	Modified	
1021	391.5	43.2	166	2	AA838792	AA838792	Recombina		1094	386.5	42.6	165	8	ADL90640	ADL90640	Human	mut
1022	391	43.1	166	8	AD032418	AD032418	Human	IFN	1095	386.5	42.6	165	8	ADL90652	ADL90652	Human	mut
1023	391	43.1	166	8	AD032414	AD032414	Human	IFN	1096	386.5	42.6	165	8	ADL90661	ADL90661	Human	mut
1024	391	43.1	166	8	AD032417	AD032417	Human	IFN	1097	386.5	42.6	165	8	ADL90636	ADL90636	Human	mut
1025	391	43.1	166	8	AD032423	AD032423	Human	IFN	1098	386.5	42.6	165	8	ADL90657	ADL90657	Human	mut
1026	391	43.1	166	8	AD032421	AD032421	Human	IFN	1099	386.5	42.6	165	8	ADL90657	ADL90657	Human	mut
1027	391	43.1	189	1	AA610017	AA610017	Sequenc		1100	386.5	42.6	165	8	ADL88822	ADL88822	Human	mod
1028	390.5	43.1	165	2	AAW43389	AAW43389	Human	int	1101	386.5	42.6	165	8	ADL88811	ADL88811	Human	mod
1029	390.5	43.1	165	8	AD125148	AD125148	Human	IFN	1102	386.5	42.6	165	8	ADL88827	ADL88827	Human	mod
1030	390.5	43.1	165	8	ADL90660	ADL90660	Human	mut	1103	386.5	42.6	165	8	ADL88806	ADL88806	Human	mod
1031	390.5	43.1	165	8	ADL90638	ADL90638	Human	mut	1104	386.5	42.6	165	1	AA660036	AA660036	Sequenc	
1032	390.5	43.1	165	8	ADL90639	ADL90639	Human	mut	1105	386	42.6	166	1	AA660036	AA660036	Sequenc	
1033	390.5	43.1	165	8	ADL88808	ADL88808	Human	mod	1106	386	42.6	166	2	AA642832	AA642832	Lymphobla	
1034	390.5	43.1	165	8	ADL88809	ADL88809	Human	mod	1107	386	42.6	166	5	AB668083	AB668083	Human	int
1035	390.5	43.1	165	8	ADL88830	ADL88830	Human	mod	1108	386	42.6	166	8	ADL88861	ADL88861	Human	cyt
1036	390	43.0	166	8	AD032400	AD032400	Human	IFN	1109	386	42.6	166	8	AD032380	AD032380	Human	int
1037	390	43.0	166	8	AD032401	AD032401	Human	IFN	1110	386	42.6	166	8	AD032406	AD032406	Human	IFN
1038	390	43.0	166	8	AD032403	AD032403	Human	IFN	1111	386	42.6	166	8	AD032407	AD032407	Human	IFN
1039	390	43.0	166	8	AD032394	AD032394	Human	IFN	1112	386	42.6	166	8	AD032307	AD032307	Human	int
1040	389.5	42.9	165	8	ADL90658	ADL90658	Human	mut	1113	386	42.6	167	1	AA630186	AA630186	Sequenc	
1041	389.5	42.9	165	8	ADL90644	ADL90644	Human	mut	1114	386	42.6	167	1	AA640130	AA640130	Sequenc	
1042	389.5	42.9	165	8	ADL90535	ADL90535	Human	mut	1115	386	42.6	189	1	AA630183	AA630183	Sequenc	
1043	389.5	42.9	165	8	ADL90673	ADL90673	Human	mut	1116	386	42.6	189	1	AA640741	AA640741	Sequenc	
1044	389.5	42.9	165	8	ADL90526	ADL90526	Human	mut	1117	386	42.6	189	1	AA640127	AA640127	Sequenc	
1045	389.5	42.9	165	8	ADL90546	ADL90546	Human	mut	1118	386	42.6	189	2	AA673231	AA673231	Porcine	i
1046	389.5	42.9	165	8	ADL90524	ADL90524	Human	mut	1119	386	42.6	189	2	AA683902	AA683902	Porcine	i
1047	389.5	42.9	165	8	ADL90614	ADL90614	Human	mut	1120	386	42.6	189	5	AB632987	AB632987	Porcine	i

1121	386	42.6	189	5	ABB0768	Human	int	1194	374.5	41.3	165	7	AD113050	Modified
1122	386	42.6	189	5	ABB07428	Interfero		1195	374.5	41.3	170	1	AAE60319	Sequence
1123	386	42.6	189	5	AAE78573	Human	int	1196	374	41.2	167	1	AAE649176	Mouse
1124	386	42.6	189	6	AAO15999	Mutant	hu	1197	373.5	41.2	150	5	ABG68840	Interfero
1125	385.5	42.5	165	8	ADL90661	Human	mut	1198	373.5	41.2	150	5	ABG68842	Interfero
1126	385.5	42.5	165	8	ADL90637	Human	mut	1199	373.5	41.2	150	5	ABG68841	Interfero
1127	385.5	42.5	165	8	ADL90653	Human	mut	1200	373.5	41.2	165	8	ADRA4609	Human
1128	385.5	42.5	165	8	ADL88823	Human	mod	1201	373.5	41.2	165	8	ADRA4608	Human
1129	385.5	42.5	165	8	ADL88831	Human	mod	1202	373.5	41.2	165	8	ADRA4595	Human
1130	385.5	42.5	165	8	ADL88807	Human	mod	1203	373.5	41.2	165	8	ADRA4598	Human
1131	385.5	42.5	165	8	ADL88813	Human	int	1204	372	41.0	133	1	AAE03038	Felis
1132	385.5	42.5	219	2	AAE11356	Alkaline		1205	372	41.0	167	4	AAE49172	Mouse
1133	385.5	42.5	165	8	ADL90589	Human	IGG	1206	371.5	41.0	165	8	ADRA4596	Human
1134	385	42.4	166	8	ADL9032405	Human	IFN	1207	371.5	41.0	396	8	ADRA4597	Human
1135	384.5	42.4	165	8	ADL90628	Human	mut	1208	371	40.9	396	1	AAE30074	Sequence
1136	384.5	42.4	165	8	ADL90635	Human	mut	1209	371	40.9	189	1	AAE73225	Bovine
1137	384.5	42.4	165	8	ADL88798	Human	mod	1210	371	40.9	189	5	AAE83896	Bovine
1138	384.5	42.4	165	8	ADL88805	Human	mod	1211	371	40.9	189	5	ABG32981	Bovine
1139	384.5	42.4	165	8	ADRA49616	Human	int	1212	370	40.8	99	2	AAE09285	Human
1140	384.5	42.4	396	8	ADRA49582	Human	IGG	1213	370	40.8	99	2	AAE44112	Human
1141	384	42.3	166	1	AAE60100	Sequence		1214	368.5	40.6	150	2	AAE11355	Interfero
1142	384	42.3	166	1	AAE90186	Hydrid	al	1215	368.5	40.6	165	5	ABG68844	Interfero
1143	383.5	42.3	165	8	ADL90551	Human	mut	1216	368	40.6	189	1	AAE50328	Bovine
1144	383.5	42.3	165	8	ADL90643	Human	mut	1217	367.5	40.5	156	8	ADL16340	Human
1145	383.5	42.3	165	8	ADL90570	Human	mut	1218	367.5	40.5	165	8	ADRA4606	Human
1146	383.5	42.3	165	8	ADL90646	Human	mut	1219	367.5	40.5	396	8	ADRA4600	Human
1147	383.5	42.3	165	8	ADL90697	Human	mut	1220	367.5	40.5	411	8	ADRA4601	Human
1148	383.5	42.3	165	8	ADL88816	Human	mod	1221	367	40.5	200	5	AAU77407	Human
1149	383.5	42.3	165	8	ADL88813	Human	mod	1222	366.5	40.4	155	8	ADL16336	Human
1150	383.5	42.3	165	8	ADL88740	Human	mod	1223	366.5	40.4	165	8	ADRA4603	Human
1151	383.5	42.3	165	8	ADL88721	Human	mod	1224	366.5	40.4	227	8	AAE47208	Human
1152	383.5	42.3	165	8	ADL88648	Human	mod	1225	365.5	40.3	165	8	ADRA4605	Human
1153	383	42.2	166	4	AAE49174	Mouse	int	1226	364	40.1	97	2	AAE09283	Human
1154	382.5	42.2	165	8	ADL90647	Human	mut	1227	364	40.1	97	2	AAE44115	Human
1155	382.5	42.2	165	8	ADL88817	Human	mod	1228	363.5	40.1	165	5	ADRA4604	Human
1156	382	42.1	189	5	ABG68073	Human	int	1229	363.5	40.1	168	5	ABG68847	Interfero
1157	381.5	42.1	165	8	ADRA4610	Human	int	1230	363	40.0	166	5	ABG68049	Feline
1158	381.5	42.1	396	8	ADRA4594	Human	IGG	1231	363	40.0	166	5	ABG68042	Feline
1159	380.5	42.0	165	8	ADRA4607	Human	int	1232	362.5	40.0	155	8	ADL16332	Human
1160	380.5	42.0	396	8	ADRA4599	Human	IGG	1233	362.5	40.0	165	7	ADL13051	Modified
1161	380	41.9	167	4	AAE49178	Mouse	int	1234	360.5	39.7	165	7	ADL13052	Modified
1162	380	41.9	189	5	ABG68074	Human	int	1235	360	39.7	189	1	AAE50326	Bovine
1163	379.5	41.8	165	8	ADRA4611	Human	int	1236	359	39.6	166	4	AAE03047	Felis
1164	379.5	41.8	396	8	ADRA4592	Human	IGG	1237	359	39.6	189	4	AAE03046	Felis
1165	378.5	41.7	159	8	ADL903410	Human	IFN	1238	358.5	39.5	151	8	ADL16328	Human
1166	378	41.7	166	4	AAE49161	Human	int	1239	358	39.5	166	3	AAE58228	Feline
1167	378	41.7	166	4	ADL88854	Human	cyt	1240	358	39.5	166	3	AAE03041	Felis
1168	378	41.7	166	8	ADL903378	Human	int	1241	358	39.5	170	1	AAE20107	Sequence
1169	378	41.7	189	1	AAE30100	Sequence		1242	358	39.5	189	3	AAE58226	Feline
1170	378	41.7	189	5	ABB07430	Interfero		1243	358	39.5	189	4	AAE03039	Felis
1171	378	41.7	189	5	AAE78565	Human	int	1244	356	39.3	99	2	AAE09284	Human
1172	378	41.7	189	6	AAO15996	Human	IFN	1245	356	39.3	166	3	AAE58227	Feline
1173	378	41.7	189	8	ADN10805	Human	int	1246	356	39.3	166	4	AAE03040	Felis
1174	378	41.7	189	8	ADN16315	Human	int	1247	356	39.3	166	4	AAE03043	Felis
1175	377.5	41.6	396	8	ADRA4591	Human	IGG	1248	356	39.3	174	8	ADL88850	Human
1176	377.5	41.6	396	8	ADRA4593	Human	IGG	1249	356	39.3	189	3	AAE58225	Feline
1177	377	41.6	161	1	AAE60305	Sequence		1250	356	39.3	189	3	AAE03038	Felis
1178	377	41.6	166	4	ADL23068	Human	int	1251	356	39.3	189	4	AAE03042	Felis
1179	377	41.6	166	4	AAE49163	Human	int	1252	355	39.1	189	1	AAE50325	Sequence
1180	377	41.6	166	8	ADL23066	Human	int	1253	353	38.9	189	1	AAE30075	Sequence
1181	377	41.6	189	1	AAE20104	Sequence		1254	353	38.9	189	2	AAE73226	Bovine
1182	377	41.6	189	6	AAO16000	Mutant	hu	1255	353	38.9	189	2	AAE83897	Bovine
1183	377	41.6	189	8	ADN10807	Human	int	1256	353	38.9	189	5	ABG32982	Bovine
1184	377	41.6	189	8	ADN16317	Human	int	1257	352.5	38.9	170	4	AAE49785	Pig
1185	376	41.5	189	2	AAE30073	Sequence		1258	352.5	38.9	170	7	ADP49377	Pig
1186	376	41.5	189	2	AAE73224	Bovine	in	1259	351	38.7	189	1	AAE50327	Bovine
1187	376	41.5	189	5	ABG32980	Bovine	in	1260	349.5	38.5	171	4	AAE03045	Felis
1188	376	41.5	189	5	ABG32980	Bovine	in	1261	349.5	38.5	171	4	AAE03044	Felis
1189	375.5	41.4	473	1	AAE60797	Interfero		1262	346.5	38.2	171	5	ABG68053	Feline
1190	375	41.3	166	4	AAE49171	Mouse	int	1263	346.5	38.0	166	5	ABG68044	Feline
1191	375	41.3	189	2	AAE22637	Murine	in	1264	345	38.0	170	2	AAE10845	Feline
1192	375	41.3	189	6	AAO16001	Mutant	hu	1265	344.5	38.0	170	2	AAE10845	Feline
1193	374.5	41.3	165	3	AAE01302	Altered	h	1266	344.5	38.0	171	5	ABG68048	Feline

1267	344.5	38.0	171	5	ABG68051	Abg68051	Feline	in	1340	289	31.9	208	3	AAy91981	AAy91981	Variant	h
1268	342	37.7	166	4	AAB49175	Aab49175	Mouse	int	1341	289	31.9	208	3	AAy92041	AAy92041	Variant	h
1269	340.5	37.5	170	4	AAG5045	Aag5045	Feline	pr	1342	289	31.9	208	5	AAE16805	AAE16805	Human	int
1270	340.5	37.5	170	5	AAE21798	Aae21798	Feline	om	1343	289	31.9	208	5	AAE16808	AAE16808	Human	int
1271	340.5	37.5	171	1	AAP90398	Aap90398	Feline	in	1344	287.5	31.7	184	1	AAp50281	AAp50281	Protein	s
1272	340.5	37.5	171	5	ABG68041	Abg68041	Feline	in	1345	287.5	31.7	184	4	AAAB49787	AAb49787	Bovine	in
1273	340.5	37.5	171	5	ABG68045	Abg68045	Feline	in	1346	287.5	31.7	186	7	ADFP94979	Adf94979	Bovine	in
1274	340.5	37.5	171	5	ABG68046	Abg68046	Feline	in	1347	287	31.6	208	3	AAy91985	AAy91985	Variant	h
1275	340.5	37.5	171	5	ABG68047	Abg68047	Feline	in	1348	287	31.6	208	5	AAE16807	AAE16807	Human	int
1276	340.5	37.5	194	1	AAP90399	Aap90399	Feline	in	1349	285	31.4	151	1	AAP80055	Aap80055	Sequence	
1277	340.5	37.5	194	7	ADE15965	Ade15965	Cat	inter	1350	282.5	31.1	165	1	AAP50280	Aap50280	Protein	s
1278	340.5	37.5	194	7	ADE15966	Ade15966	Cat	inter	1351	282.5	31.1	186	1	AAp30078	AAp30078	Sequence	
1279	340	37.5	166	4	AAB49177	Aab49177	Mouse	int	1352	282.5	31.1	186	2	AAAB73229	AAb73229	Bovine	in
1280	335	36.9	167	1	AAP30223	Aap30223	Sequence		1353	282.5	31.1	186	5	AAAB39900	AAb39900	Bovine	in
1281	335	36.9	167	1	AAP60689	Aap60689	Hybrid	pr	1354	282.5	31.1	186	5	ABG32985	Abg32985	Bovine	le
1282	334.5	36.9	170	2	AAW58568	Aaw58568	Amino	aci	1355	280	30.9	193	3	AAy91979	AAy91979	Truncated	
1283	334.5	36.9	170	2	AAy07474	Aay07474	Recombina		1356	280	30.9	193	3	AAy91977	AAy91977	Variant	h
1284	333.5	36.8	171	5	ABG68043	Abg68043	Feline	in	1357	280	30.9	193	5	AAE16801	AAE16801	Human	int
1285	333.5	36.8	171	5	ABG68050	Abg68050	Feline	in	1358	280	30.9	193	5	AAE16799	AAE16799	Human	int
1286	333	36.7	167	7	ADFI17016	Adfi17016	Human	alb	1359	280	30.9	193	6	ABU62228	Abu62228	Human	int
1287	333	36.7	167	7	ADH22026	Adh22026	Human	IFN	1360	280	30.9	193	6	ABU62231	Abu62231	Human	int
1288	332.5	36.7	172	5	ABB07441	Abb07441	Interfero		1361	277	30.5	161	2	AAy25092	AAy25092	Synthetic	
1289	332	36.6	95	2	AAW09286	Aaw09286	Human	mat	1362	277	30.5	161	6	AAO30310	Aao30310	Human	int
1290	332	36.6	95	2	AAW44113	Aaw44113	Human	int	1363	277	30.5	192	3	AAy91978	AAy91978	Truncated	
1291	331.5	36.5	162	4	AAB49173	Aab49173	Mouse	int	1364	277	30.5	192	5	AAE16800	AAE16800	Human	int
1292	331.5	36.5	166	1	AAP80050	Aap80050	Sequence		1365	275	30.5	192	6	ABU62229	Abu62229	Human	int
1293	330.5	36.4	166	1	AAP30222	Aap30222	Sequence		1366	275	30.4	331	1	AAp70170	AAp70170	Sequence	
1294	330.5	36.4	166	1	AAP60688	Aap60688	Hybrid	pr	1367	273	30.1	166	1	AAPE50025	AAPE50025	Sequence	
1295	330.5	36.4	166	7	ADFI17017	Adfi17017	Human	alb	1368	272.5	30.0	166	1	AAPE50030	AAPE50030	Sequence	
1296	330.5	36.4	166	7	ADH22027	Adh22027	Human	IFN	1369	270.5	29.8	166	1	AAPE50274	AAPE50274	Protein	s
1297	329	36.3	167	1	AAP80051	Aap80051	Sequence		1370	270.5	29.8	166	1	AAPE50028	AAPE50028	Sequence	
1298	321	35.4	165	1	AAP50273	Aap50273	Protein	s	1371	270.5	29.8	166	1	AAp70169	AAp70169	Sequence	
1299	319	35.2	157	5	ABG68060	Abg68060	Human	int	1372	269.5	29.7	166	1	AAPE50029	AAPE50029	Sequence	
1300	318	35.1	166	1	AAP50270	Aap50270	Protein	s	1373	268.5	29.6	166	1	AAPE50031	AAPE50031	Sequence	
1301	316	34.8	187	1	AAP60401	Aap60401	Canine	IF	1374	267.5	29.5	166	1	AAPE50022	AAPE50022	Sequence	
1302	316	34.8	187	1	AAP60402	Aap60402	Canine	IF	1375	265.5	29.3	166	1	AAPE50024	AAPE50024	Sequence	
1303	313	34.5	166	1	AAP50275	Aap50275	Protein	s	1376	264.5	29.2	165	1	AAPE50207	AAPE50207	Modified	
1304	312	34.4	132	6	ABU52320	Abu52320	Human	GPC	1377	264.5	29.2	166	1	AAPE50194	AAPE50194	Modified	
1305	312	34.4	132	6	ADL23975	Adl23975	Human	NOV	1378	264.5	29.2	166	1	AAPE50196	AAPE50196	Modified	
1306	312	34.4	151	6	ABU52319	Abu52319	Human	GPC	1379	264.5	29.2	166	1	AAPE50023	AAPE50023	Sequence	
1307	312	34.4	151	6	ADL23973	Adl23973	Human	NOV	1380	264	29.1	90	3	AAy55967	Aay55967	Partial	h
1308	311	34.3	166	4	AAG61825	Aag61825	Interfero		1381	263.5	29.1	166	1	AAPE50272	AAPE50272	Protein	s
1309	311	34.3	166	8	AD129653	Ad129653	Human	int	1382	263.5	29.1	166	1	AAPE50206	AAPE50206	Modified	
1310	308	34.0	166	1	AAP50276	Aap50276	Protein	s	1383	263.5	29.1	166	1	AAPE50193	AAPE50193	Modified	
1311	307	33.8	155	8	AAP30227	Aap30227	Sequence		1384	263.5	29.1	166	1	AAPE50027	AAPE50027	Sequence	
1312	307	33.3	155	8	ADSL6329	Adsl6329	Human	int	1385	263.5	29.1	166	8	ADL89875	Adl89875	Human	mut
1313	301	33.2	156	8	ADSL6341	Adsl6341	Human	int	1386	263.5	29.1	166	8	ADL90985	Adl90985	Human	mut
1314	300	33.1	155	8	ADSL6337	Adsl6337	Human	int	1387	263.5	29.1	166	8	ADL89849	Adl89849	Human	mod
1315	296	32.6	155	8	ADSL6333	Adsl6333	Human	int	1388	263.5	29.1	166	8	ADL89959	Adl89959	Human	mod
1316	294	32.4	208	3	AAy91986	AAy91986	Human	int	1389	262	28.9	180	8	ADN10826	Adn10826	Human	int
1317	294	32.4	208	3	AAy91982	AAy91982	Variant	h	1390	261.5	28.8	166	8	ADL90748	Adl90748	Human	mut
1318	294	32.4	208	5	AAE16796	Aae16796	Human	int	1391	261.5	28.8	166	8	ADL89722	Adl89722	Human	mod
1319	294	32.4	208	5	AAE16796	Aae16796	Human	int	1392	261	28.8	166	8	ADN10825	Adn10825	Human	int
1320	294	32.4	208	6	ABU62225	Abu62225	Human	int	1393	260.5	28.7	166	1	AAPE50271	AAPE50271	Protein	s
1321	293	32.3	120	5	ABBO4303	Abb04303	Recombina		1394	260.5	28.6	166	1	ADL88902	Adl88902	Human	mod
1322	293	32.3	120	8	ADQ87760	Adq87760	Super-com		1395	259.5	28.6	166	8	AAPE50278	AAPE50278	Protein	s
1323	292	32.2	166	1	AAP50277	Aap50277	Protein	s	1396	259.5	28.6	166	8	ADL90862	Adl90862	Human	mut
1324	291	32.1	208	3	AAy91983	AAy91983	Variant	h	1397	259.5	28.6	166	8	ADL90876	Adl90876	Human	mut
1325	291	32.1	208	5	AAE16806	Aae16806	Human	int	1398	259.5	28.6	166	8	ADL89850	Adl89850	Human	mod
1326	290	32.0	161	1	AAP60691	Aap60691	Hybrid	pr	1399	259.5	28.6	166	4	ADL89836	Adl89836	Human	mod
1327	290	32.0	208	1	AAy06311	Aay06311	Human	int	1400	259	28.6	166	4	AAAB49371	AAb49371	Human	INF
1328	290	32.0	208	3	AAy71466	AAy71466	Human	PRO	1401	258.5	28.5	166	1	AAPE50032	AAPE50032	Sequence	
1329	290	32.0	208	3	AAy91984	AAy91984	Variant	h	1402	258.5	28.5	166	1	AAPE80047	AAPE80047	Sequence	
1330	290	32.0	208	3	AAy91980	AAy91980	Human	int	1403	258.5	28.5	166	8	ADL90749	Adl90749	Human	mut
1331	290	32.0	208	5	AAE16795	Aae16795	Human	int	1404	258.5	28.5	166	8	ADL90915	Adl90915	Human	mut
1332	290	32.0	208	5	ABBO7424	Abb07424	Interfero		1405	258.5	28.5	166	8	ADL90895	Adl90895	Human	mut
1333	290	32.0	208	5	ABBO7426	Abb07426	Interfero		1406	258.5	28.5	166	8	ADL89723	Adl89723	Human	mod
1334	290	32.0	208	5	AAE16795	Aae16795	Human	int	1407	258.5	28.5	166	8	ADL89869	Adl89869	Human	mod
1335	290	32.0	208	6	ABU62224	Abu62224	Human	int	1408	258.5	28.5	166	8	ADL89889	Adl89889	Human	mod
1336	290	32.0	208	6	ADN10816	Adn10816	Human	PRO	1409	257.5	28.4	166	4	ABU09811	ABU09811	Human	int
1337	290	32.0	208	8	ADN10816	Adn10816	Human	int	1410	257.5	28.4	166	4	ABAB49378	ABa49378	Human	INF
1338	290	32.0	208	8	ADSL6326	Adsl6326	Human	int	1411	257.5	28.4	166	4	AAU00130	AAU00130	Human	int
1339	290	32.0	215	7	ADML3725	Adml3725	Human	int	1412	257.5	28.4	166	4	AAU00112	AAU00112	Human	int

1413	257.5	28.4	166	4	AAU00149	AAU00149	Human	int
1414	257.5	28.4	166	4	AAU00156	AAU00156	Human	int
1415	257.5	28.4	166	4	AAU00155	AAU00155	Human	int
1416	257.5	28.4	166	4	AAU00135	AAU00135	Human	int
1417	257.5	28.4	166	6	ABR40020	ABR40020	Mutant	in
1418	257.5	28.4	166	8	ADJ56143	ADJ56143	Human	int
1419	257.5	28.4	166	8	ADJ90734	ADJ90734	Human	int
1420	257.5	28.4	166	8	ADJ90758	ADJ90758	Human	int
1421	257.5	28.4	166	8	ADJ90882	ADJ90882	Human	int
1422	257.5	28.4	166	8	ADJ97877	ADJ97877	Human	int
1423	257.5	28.4	166	8	ADJ98708	ADJ98708	Human	mod
1424	257.5	28.4	166	8	ADJ98956	ADJ98956	Human	mod
1425	257.5	28.4	166	8	ADJ88921	ADJ88921	Human	mod
1426	257.5	28.4	166	8	ADJ88914	ADJ88914	Human	mod
1427	257.5	28.4	166	8	ADJ89668	ADJ89668	Human	mod
1428	257.5	28.4	166	8	ADJ89732	ADJ89732	Human	int
1429	257.5	28.4	166	8	ADJ10820	ADJ10820	Human	int
1430	257	28.3	166	4	ABAB4369	ABAB4369	Human	int
1431	257	28.3	166	8	ADJ90852	ADJ90852	Human	int
1432	257	28.3	166	8	ADJ89826	ADJ89826	Human	int
1433	257	28.3	186	1	AAE60398	AAE60398	Human	mod
1434	257	28.3	186	5	AAE23000	AAE23000	Ergline	IF
1435	257	28.3	186	5	AAE29001	AAE29001	Ergline	int
1436	256.5	28.3	165	8	ADJ90735	ADJ90735	Human	mod
1437	256.5	28.3	165	8	ADJ89709	ADJ89709	Human	mod
1438	256.5	28.3	166	1	AAE50526	AAE50526	Sequence	
1439	256.5	28.3	166	2	AAE06574	AAE06574	Human	int
1440	256.5	28.3	166	2	AAW47192	AAW47192	Interfero	
1441	256.5	28.3	166	4	AAU00085	AAU00085	Human	int
1442	256.5	28.3	166	4	AAU00071	AAU00071	Human	int
1443	256.5	28.3	166	4	AAU00157	AAU00157	Human	int
1444	256.5	28.3	166	4	AAU00086	AAU00086	Human	int
1445	256.5	28.3	166	6	ABP72809	ABP72809	Human	int
1446	256.5	28.3	166	8	ADJ90779	ADJ90779	Human	int
1447	256.5	28.3	166	8	ADJ90877	ADJ90877	Human	int
1448	256.5	28.3	166	8	ADJ88949	ADJ88949	Human	mod
1449	256.5	28.3	166	8	ADJ89753	ADJ89753	Human	mod
1450	256.5	28.3	166	8	ADJ89851	ADJ89851	Human	mod
1451	256.5	28.3	166	8	ADJ89666	ADJ89666	Human	mod
1452	256.5	28.3	166	8	ADJ88903	ADJ88903	Human	mod
1453	256.5	28.3	369	5	AAU99389	AAU99389	Mutant	hu
1454	256	28.2	166	4	ABAB4370	ABAB4370	Human	int
1455	256	28.2	166	8	ADJ90832	ADJ90832	Human	int
1456	256	28.2	166	8	ADJ90833	ADJ90833	Human	int
1457	256	28.2	166	8	ADJ90823	ADJ90823	Human	int
1458	256	28.2	166	8	ADJ89806	ADJ89806	Human	mod
1459	256	28.2	166	8	ADJ89797	ADJ89797	Human	mod
1460	255.5	28.2	166	4	AAU00080	AAU00080	Human	int
1461	255.5	28.2	166	4	AAU00114	AAU00114	Human	int
1462	255.5	28.2	166	4	AAU00082	AAU00082	Human	int
1463	255.5	28.2	166	4	AAU00082	AAU00082	Human	int
1464	255.5	28.2	166	6	ABP72808	ABP72808	Human	int
1465	255.5	28.2	166	8	ADJ90743	ADJ90743	Human	mod
1466	255.5	28.2	166	8	ADJ90912	ADJ90912	Human	mod
1467	255.5	28.2	166	8	ADJ90767	ADJ90767	Human	mod
1468	255.5	28.2	166	8	ADJ90746	ADJ90746	Human	mod
1469	255.5	28.2	166	8	ADJ90878	ADJ90878	Human	mod
1470	255.5	28.2	166	8	ADJ90782	ADJ90782	Human	mod
1471	255.5	28.2	166	8	ADJ90851	ADJ90851	Human	mod
1472	255.5	28.2	166	8	ADJ88912	ADJ88912	Human	mod
1473	255.5	28.2	166	8	ADJ88911	ADJ88911	Human	mod
1474	255.5	28.2	166	8	ADJ89720	ADJ89720	Human	mod
1475	255.5	28.2	166	8	ADJ89717	ADJ89717	Human	mod
1476	255.5	28.2	166	8	ADJ89741	ADJ89741	Human	mod
1477	255.5	28.2	166	8	ADJ89852	ADJ89852	Human	mod
1478	255.5	28.2	166	8	ADJ89886	ADJ89886	Human	mod
1479	255.5	28.2	166	8	ADJ89896	ADJ89896	Human	mod
1480	255.5	28.2	166	8	ADJ88913	ADJ88913	Human	mod
1481	255.5	28.2	166	8	ADJ88950	ADJ88950	Human	mod
1482	255.5	28.2	166	8	ADJ89756	ADJ89756	Human	mod
1483	255.5	28.2	166	8	ADJ89825	ADJ89825	Human	mod
1484	255.5	28.2	423	3	ADJY0869	ADJY0869	Human	int
1485	255.5	28.2	423	3	AAV50907	AAV50907	VCM	sign

1486	255.5	28.2	423	8	AA043336	Ado43396	Amino aci
1487	255	28.1	166	4	AA049368	Ado49368	Human INF
1488	255	28.1	166	8	ADL90828	Adl90828	Human mut
1489	255	28.1	166	8	ADL90835	Adl90835	Human mut
1490	255	28.1	166	8	ADL90867	Adl90867	Human mut
1491	255	28.1	166	8	ADL89802	Adl89802	Human mod
1492	255	28.1	166	8	ADL89809	Adl89809	Human mod
1493	255	28.1	166	8	ADL89841	Adl89841	Human mod
1494	255	28.1	180	8	ADN10829	Adn10829	Human int
1495	255	28.1	186	1	AA030079	Aaw30079	Sequence
1496	255	28.1	186	2	AAW73230	Aaw73230	Bovine in
1497	255	28.1	186	2	AAW83901	Aaw83901	Bovine in
1498	255	28.1	186	5	ABG32986	Abg32986	Bovine 1e
1499	255	28.1	775	7	ADFI14951	Adfi14951	Human alb
1500	255	28.1	775	7	ADH21287	Adh21287	Human alb

ALIGNMENTS

RESULT 1

AA054768

AA054768 standard; protein; 172 AA.

XX

AC

AA054768;

XX

DT

25-MAR-2003 (revised)

XX

DT

01-DEC-1994 (first entry)

XX

DE

Sheep interferon-tau mature protein.

XX

KW

Sheep; interferon-tau; immunostimulant; antitumor; virucide.

XX

OS

Ovis aries.

XX

XX

MO9410313-A2.

XX

PD

11-MAY-1994.

XX

PE

19-OCT-1993; 93MO-US010016.

XX

PR

30-OCT-1992; 92US-00969890.

XX

XX

(UYFL) UNIV FLORIDA.

XX

PA

(WOME-) WOMEN'S RES INST.

XX

PI

Bazer FW, Johnson HM, Pontzer CH, Ott TL, Van Heeke G, Imakawa K;

XX

DR

WPI; 1994-167468/20.

XX

DR

N-PSDB; AA064824.

XX

PT

Interferon tau compans - lacking cytotoxic side effects when used as

XX

PS

antivirals, and anti:cellular proliferation agents.

XX

PS

Claim 3; Page 90; 126pp; English.

XX

CC

This sheep INF-tau protein is expressed in yeast, insect cells or E. coli

XX

CC

using expression vector phage lambda-gtl1. The protein is useful for

XX

CC

inhibitin tumor cell growth, for inhibiting vital replication in cells

XX

CC

and enhancing fertility in female mammals. (Updated on 25-MAR-2003 to

XX

CC

correct PW field.)

XX

XX

Sequence 172 AA:

Query Match 100.0%; Score 907; DB 2; Length 172;

Best Local Similarity 100.0%; Pred. No. 1e-92;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0

1 CYLSRKMLDLDRNWKLLDRNKRLLSPHSCLDPRKDFGLPQEWVEEDLOLQKDAFPVLYEM 60

1 CYLSRKMLDLDRNWKLLDRNKRLLSPHSCLDPRKDFGLPQEWVEEDLOLQKDAFPVLYEM 60

61 LOQSFNLFYTHSSAAMDITLLLEQLCTGLQOQLDLDTCRGQVMEEDSELGNDMPITVY 120

Db 61 LOOSFNLFTYEHSSAAMDITLLBOLCTGLQOQLDHLDTGCGQVWGEEDSELGNMDDPIVTV 120
 QY 121 KKVFQGIYDYLOEKGYSDCAMEIVRVMEMRALTVSTTLQKRLTRMGDGLNSP 172
 Db 121 KKVFQGIYDYLOEKGYSDCAMEIVRVMEMRALTVSTTLQKRLTRMGDGLNSP 172

RESULT 2

AAR99397
 ID AAR99397 standard; protein; 172 AA.

AC AAR99397;

DT 29-DEC-1996 (first entry)

DE Ovine tau interferon (synthetic).

XX Tau interferon; ovine; bovine; autoimmune disease;

KM proliferative disorder; viral disease; fertility.

XX Synthetic.

XX WO9628183-A1.

XX 19-SEP-1996.

PF 15-MAR-1996; 96WO-US003472.

PR 16-MAR-1995; 95US-00406190.

XX (UYFL) UNIV FLORIDA.

PI Soos JM, Schiffenbauer J, Johnson HM;

XX WPI; 1996-464609/46.

DR N-PSDB; AAT41504.

XX Tau interferon-concg. medicament - useful to treat autoimmune diseases,

PT proliferative disorder, viral diseases or to enhance fertility in a

XX female mammal.

XX Claim 5; Page 48; 65pp; English.

CC Ovine and human tau interferon may be used in medicaments to treat

CC autoimmune disorders (e.g. multiple sclerosis or rheumatoid arthritis), a

CC proliferative disorder (e.g. cancer) or a viral disease (e.g. hepatitis

CC B). It can also be used to enhance fertility in female mammals. The

CC medicament is given orally or by injection. Ovine and human tau

CC interferon sequences are given in AAT41504 to AAT41506

XX

XX

QY 1 CYLSRKMLDARENLKLLDRNRLSPHSCLODRKDFGLPEWVGGDLOKQOAFPPVLYEM 60

Db 1 CYLSRKMLDARENLKLLDRNRLSPHSCLODRKDFGLPEWVGGDLOKQOAFPPVLYEM 60

QY 61 LOOSFNLFTYEHSSAAMDITLLBOLCTGLQOQLDHLDTGCGQVWGEEDSELGNMDDPIVTV 120

Db 61 LOOSFNLFTYEHSSAAMDITLLBOLCTGLQOQLDHLDTGCGQVWGEEDSELGNMDDPIVTV 120

QY 121 KKVFQGIYDYLOEKGYSDCAMEIVRVMEMRALTVSTTLQKRLTRMGDGLNSP 172

Db 121 KKVFQGIYDYLOEKGYSDCAMEIVRVMEMRALTVSTTLQKRLTRMGDGLNSP 172

RESULT 3
 AAW31698
 ID AAW31698 standard; protein; 172 AA.

XX AAW31698;
 AC 14-APR-1998 (first entry)
 DT Mature ovine interferon-tau (OviFNtau) protein.
 DE Mature ovine interferon-tau (OviFNtau) protein.
 XX Interferon-tau; ovine; human; autoimmune disease; treatment; toxicity;
 KM IFN tau; multiple sclerosis; diabetes mellitus; asthma; allergy; cancer.
 XX

OS Ovis aries.

XX WO9733607-A1.

XX 18-SEP-1997.

PF 12-MAR-1997; 97WO-US003794.

PR 15-MAR-1996; 96US-00616904.

XX (UYFL) UNIV FLORIDA.

PA Soos JM, Schiffenbauer J, Johnson HM;

XX WPI; 1997-470642/43.

DR N-PSDB; AAV02288.

PT Oral administration of interferon-tau for treatment of auto-immune

PT disease - avoids toxicity of interferon alpha and generates fewer

PT specific antibodies than injection.

XX Claim 5; Page 31; 48pp; English.

XX This is a mature ovine interferon-tau (OviFNtau) protein. The ovine and

CC the human interferon-tau (IFN tau) can be used in the treatment of

CC mammalian diseases responsive to IFN tau. The new feature in the

CC treatment is that IFN tau is administered orally. The method is used to

CC treat immune, particularly autoimmune disease, specifically multiple

CC sclerosis (a preferred application, reducing both severity and frequency

CC of relapses), type I diabetes mellitus, lupus erythematosus, amyotrophic

CC lateral sclerosis, Crohn's disease, rheumatoid arthritis, stomatitis,

CC asthma, allergies and psoriasis, particularly in humans or dogs. IFN tau

CC is also useful for treating cancer (e.g. hairy cell leukaemia, Kaposi's

CC sarcoma and multiple myeloma), cell proliferation and viral diseases

CC (hepatitis, human immunodeficiency virus etc., including prevention of

CC maternal transmission). It is also used for increasing fertility in

CC female mammals (increasing life time of the corpus luteum). Oral

CC administration is as effective as injection but is more convenient and

CC generates a lower level of anti-IFN tau antibodies. Use of IFN tau avoids

CC the toxicity associated with use of IFN alpha

XX

QY 1 CYLSRKMLDARENLKLLDRNRLSPHSCLODRKDFGLPEWVGGDLOKQOAFPPVLYEM 60

Db 1 CYLSRKMLDARENLKLLDRNRLSPHSCLODRKDFGLPEWVGGDLOKQOAFPPVLYEM 60

QY 61 LOOSFNLFTYEHSSAAMDITLLBOLCTGLQOQLDHLDTGCGQVWGEEDSELGNMDDPIVTV 120

Db 61 LOOSFNLFTYEHSSAAMDITLLBOLCTGLQOQLDHLDTGCGQVWGEEDSELGNMDDPIVTV 120

QY 121 KKVFQGIYDYLOEKGYSDCAMEIVRVMEMRALTVSTTLQKRLTRMGDGLNSP 172

Db 121 KKVFQGIYDYLOEKGYSDCAMEIVRVMEMRALTVSTTLQKRLTRMGDGLNSP 172

RESULT 4
 AAW44110
 ID AAW44110 standard; protein; 172 AA.

XX AAM44110;
 AC 16-JUN-1998 (first entry)
 XX
 XX
 XX
 XX Mature ovine interferon tau.
 DE
 XX Hybrid fusion; interferon-tau; inhibits tumour; viral growth; IFN-
 KM autoimmune disease; immune response.
 XX
 XX Ovis aries.
 OS
 XX MO9739127-A1.
 PN
 XX 23-OCT-1997.
 PD
 XX 11-APR-1997; 97WO-US006114.
 PF
 XX 12-APR-1996; 96US-0061328.
 PR
 XX (UYFL) UNIV FLORIDA.
 PA
 XX Johnson HM, Subramaniam PS, Pontzer CH;
 PI MPI: 1997-526463/48.
 XX N-PSDB; AAV02178.
 DR
 XX
 XX Hybrid nucleic acid encodes fusion of interferon-tau and other interferon
 PT - used to inhibit tumour and viral growth, and for treating auto-immune
 PT disease, less toxic than native type I interferon.
 XX
 XX Disclosure, Page 83; 147pp; English.
 PS
 XX The present sequence represents mature ovine interferon tau from the
 CC present invention. The present invention describes a novel chimeric
 CC nucleic acid which comprises: (i) a 5'-segment encoding the N-terminal
 CC amino acid (aa) sequence of an interferon tau (IFN τ) polypeptide; and
 CC (ii) a 3'-sequence encoding the C-terminal aa sequence of a non-tau type
 CC I interferon, with the two segments spliced in a region comprising part
 CC of the mature interferon between residues 8 and 37. Hybrid interferon
 CC fusion polypeptides are used to inhibit tumour growth (e.g. of steroid-
 CC sensitive tumours) and viral replication (e.g. of human immunodeficiency
 CC virus, hepatitis B or C virus, feline leukaemia virus) and to treat
 CC autoimmune diseases (e.g. lupus erythematosus, type I diabetes,
 CC rheumatoid arthritis). Some hybrid interferon fusion polypeptides may
 CC block the antiviral/antiproliferative actions of IFN τ , so can be used to
 CC prevent immune responses induced by interferons, e.g. in organ
 CC transplantation. The hybrid interferon fusion polypeptides can also be
 CC used to raise antibodies, used e.g. for analysis of structure/function
 CC relationships. The novel chimeric nucleic acid is used to produce
 CC recombinant hybrid interferon fusion polypeptides. Hybrid interferon
 CC fusion polypeptides are less toxic than type I interferons, so can be
 CC administered at higher doses
 CC
 XX
 XX Sequence 172 AA;
 SQ
 Query Match 100.0%; Score 907; DB 2; Length 172;
 Best Local Similarity 100.0%; Pred. No. 1e-92;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 ABB07588
 ID ABB07588 standard; protein; 172 AA.
 XX
 XX
 XX ABB07588;
 AC
 XX 08-MAY-2002 (first entry)
 DT
 XX
 XX Ovine interferon-tau protein.
 DE
 XX Hepatitis C virus; HCV infection; ovine; interferon-tau; ovIFN-tau; OAS;
 KM 2',5'-oligoadenylate synthetase; virucide; hepatotropic; IFN-tau.
 XX
 XX Ovis aries.
 OS
 XX MO200206343-A2.
 PN
 XX 24-JAN-2002.
 PD
 XX 19-JUL-2001; 2001WO-US022976.
 PF
 XX 19-JUL-2000; 2000US-0219128P.
 PR 17-OCT-2000; 2000JP-00317160.
 XX
 XX (PEPG-) PEPGEN CORP.
 PA
 XX Sokawa Y, Liu C;
 PI MPI: 2002-179784/23.
 XX N-PSDB; ABA94936.
 DR
 XX
 XX Oral-delivery composition for treating conditions relating to hepatitis
 PT caused by hepatitis C virus, comprises ovine interferon-tau which
 PT stimulates bloodstream levels of 2',5'-oligoadenylate synthetase.
 PT
 XX
 XX Example 1; Page 32-33; 33pp; English.
 PS
 XX The invention provides an oral-delivery composition for use in treating
 CC hepatitis C virus (HCV) in a HCV-infected patient. The composition
 CC comprises ovine interferon-tau (ovIFN-tau), in a dosage effective to
 CC stimulate bloodstream levels of 2',5'-oligoadenylate synthetase (OAS).
 CC The ovIFN-tau synthesizes OAS which degrades viral mRNA. A method is also
 CC provided for monitoring the treatment of HCV by oral administration of
 CC ovIFN-tau, by measuring the blood levels of OAS prior to and after such
 CC oral administration, and if necessary, adjusting the dose of IFN-tau
 CC until a measurable increase in blood OAS level, relative to the level
 CC observed prior to administration. The composition is useful for treating
 CC hepatitis caused by HCV and the method is useful for monitoring treatment
 CC of HCV by oral administration of ovIFN-tau. The present sequence
 CC represents an ovine interferon-tau protein
 CC
 XX
 XX Sequence 172 AA;
 SQ
 Query Match 100.0%; Score 907; DB 5; Length 172;
 Best Local Similarity 100.0%; Pred. No. 1e-92;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

XX AC AD117857;
XX XX
XX 22-APR-2004 (first entry)
XX DE Mature ovine interferon-tau, SEQ ID NO:2.
XX
XX Interferon-tau; oral dosage form; oral administration; fasted state;
XX 2',5'-oligoadenylate synthetase; OAS; autoimmune condition;
XX multiple sclerosis; diabetes mellitus; Hashimoto's thyroiditis;
XX rheumatoid arthritis; uveitis; psoriasis; systemic lupus erythematosus;
XX allergy; asthma; eczema; Crohn's disease; ulcerative colitis;
XX viral infection; HIV infection; hepatitis;
XX cellular proliferation disorder; multiple myeloma; ovarian cancer;
XX hairy cell leukemia; inflammatory disease; immunosuppressive; virucide;
XX cytostatic; antiinflammatory; neuroprotective; antidiabetic;
XX thymomimetic; antirheumatic; antiarthritic; ophthalmological;
XX antiporiatic; dermatological; antiallergic; antisthmatic; antilucer;
XX anti-HIV; hepatotropic; vaccine; ovine; sheep.
XX
XX Ovis aries.
XX OS Synthetic.
XX
XX MO2003061728-A2.
XX
XX 31-JUL-2003.
XX
XX 16-JAN-2003; 2003WO-US001596.
XX
XX 16-JAN-2002; 2002US-0349658P.
XX
XX (PEPG-) PEPGEN CORP.
XX
XX Sokawa Y, Liu C;
XX
XX WPI; 2003-598711/56.
XX
XX N-PSDB; AD117856.
XX
XX An oral dosage form of interferon-tau administered to a subject in a
XX fasted state to achieve an increased level of 2',5'-oligoadenylate
XX synthetase, useful for treating a condition responsive to interferon-tau,
XX e.g. viral infection.
XX
XX Claim 3; SEQ ID NO 2; 28pp; English.
XX
XX The invention relates to a composition for use in treating a condition
XX responsive to interferon-tau, comprising an oral dosage form of interfeon
XX -tau. The composition is administered to a patient in a fasted state to
XX increase the level of 2',5'-oligoadenylate synthetase (OAS) in the blood
XX relative to that obtained after administration of interferon-tau to a fed
XX patient. The interferon-tau used in the composition is preferably ovine
XX or bovine. The composition is useful in the treatment of autoimmune
XX conditions (e.g., multiple sclerosis, diabetes mellitus, Hashimoto's
XX thyroiditis, rheumatoid arthritis, uveitis, psoriasis, systemic lupus
XX erythematosus, allergies, asthma, eczema, Crohn's disease or ulcerative
XX colitis), viral infections (e.g., HIV infection or hepatitis), disorders
XX associated with cellular proliferation (e.g., multiple myeloma, ovarian
XX cancer or hairy cell leukemia), or inflammatory diseases. The present
XX sequence represents mature ovine interferon-tau.
XX
XX Sequence 172 AA;
XX
XX Query Match 100.0%; Score 907; DB 7; Length 172;
XX Best Local Similarity 100.0%; Pred. NO. 1e-92;
XX Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 121 KKYFGGIYDYLOEKGYSDCAMEIVRVMNRALTIVSTTLQKRLTMGGDINSF 172
DB 121 KKYFGGIYDYLOEKGYSDCAMEIVRVMNRALTIVSTTLQKRLTMGGDINSF 172
XX
XX RESULT 7
XX ID ADM79177 standard; protein; 172 AA.
XX
XX ADM79177;
XX
XX 15-JUL-2004 (first entry)
XX
XX Mature ovine interferon tau protein SEQ ID NO:1.
XX
XX oral administration; interferon; IFN; ovine; mature interferon tau.
XX
XX Ovis aries.
XX OS
XX
XX MO2004032863-A2.
XX
XX 22-APR-2004.
XX
XX 08-OCT-2003; 2003WO-US031999.
XX
XX 09-OCT-2002; 2002US-0417292P.
XX
XX (PEPG-) PEPGEN CORP.
XX
XX Manning MC, Nayar R;
XX
XX WPI; 2004-340799/31.
XX
XX A composition for oral administration of an interferon (IFN) comprises an
XX IFN and a species that stabilizes the IFN in an active form by
XX interaction between the interferon and the species.
XX
XX Example; SEQ ID NO 1; 52pp; English.
XX
XX The present invention describes a composition for the oral administration
XX of an interferon (IFN) comprising an IFN and a species that stabilizes
XX the IFN in an active form by interaction between the IFN and the species.
XX Also described: (1) preparing a protein for oral administration,
XX comprising formulating the protein with a species that stabilizes the
XX protein in an active form by binding interaction between the protein and
XX the species, therefore the formulating results in a composition for oral
XX administration; and (2) selecting a dosage form composition for a protein
XX that achieves protein stabilisation for biological activity upon in vivo
XX administration, comprising selecting a protein for formulation, preparing
XX solutions of the selected protein or polypeptide in different buffers at
XX different pH values, and measuring the effect of the buffer on the
XX protein's tertiary structure, where the measuring identifies buffers that
XX result retention of the protein's tertiary structure. The composition and
XX methods are useful for preparing oral dosage forms for administration of
XX proteins and polypeptides. The present sequence represents the mature
XX ovine interferon tau amino acid sequence, which is used in an example
XX from the present invention.
XX
XX Sequence 172 AA;
XX
XX Query Match 100.0%; Score 907; DB 8; Length 172;
XX Best Local Similarity 100.0%; Pred. NO. 1e-92;
XX Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 121 KKYFGIYDYLQEKGYSDCAMEIIVVENMRALTIVSTTLQKRLTKMGDLNSP 172
 DB 121 KKYFGIYDYLQEKGYSDCAMEIIVVENMRALTIVSTTLQKRLTKMGDLNSP 172

RESULT 8
 ADS13613
 ID ADS13613 standard; protein; 172 AA.
 AC ADS13613;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Sheep interferon tau begid 2.
 XX
 KW immunosuppressive; cytotatic; virucide; neuroprotective; antidiabetic;
 KW muscular; antiinflammatory; antirheumatic; antiarthritic; antiaesthetic;
 KW dermatological; vaccine; interferon tau; 2',5'-oligoadenylate synthetase;
 KW OAS; autoimmune condition; cancer; viral infection; multiple sclerosis;
 KW hepatitis C infection; diabetes mellitus; systemic lupus erythematosus;
 KW amyotrophic lateral sclerosis; Crohn's disease; rheumatoid arthritis;
 KW aethma; uveitis; psoriasis; hypersensitivity disorder; sheep.
 KW
 OS Ovis aries.
 XX
 PN US2004191217-A1.
 XX
 PD 30-SEP-2004.
 XX
 PE 21-NOV-2003; 2003US-00719472.
 XX
 PR 19-JUL-2000; 2000US-0219128P.
 PR 19-JUL-2001; 2001US-00910406.
 PR 16-JAN-2002; 2002US-0349658P.
 PR 16-JAN-2003; 2003US-00346269.
 PR 31-OCT-2003; 2003US-00698927.
 XX
 PA (SOKA/) SOKAMA Y.
 PA (LIUC/) LIU C.
 XX
 PI Sokawa Y, Liu C;
 XX
 DR WPI; 2004-698654/68.
 DR N-PSDB; ADS13612.
 XX
 PT Treating a condition in a subject, e.g. autoimmune condition, cancer or
 PT viral infection, comprises orally administering interferon-tau to the
 PT intestinal tract to increase the blood 2'5'-oligoadenylate synthetase
 PT level.
 XX
 PS Claim 2; SEQ ID NO 2; 38pp; English.
 XX
 CC The invention describes a method of treating a condition in a human
 CC subject responsive to interferon tau therapy comprises orally
 CC administering interferon-tau to the intestinal tract of the subject to
 CC produce an initial measurable increase in the subject's blood 2',5'-
 CC oligoadenylate synthetase (OAS) level, relative to the blood OAS level in
 CC the subject in the absence of interferon-tau administration. The method
 CC is useful for treating an autoimmune condition, cancer, or a viral
 CC infection. The method is particularly useful for treating multiple
 CC sclerosis or hepatitis C infection, diabetes mellitus, systemic lupus
 CC erythematosus, amyotrophic lateral sclerosis, Crohn's disease, rheumatoid
 CC arthritis, aethma, uveitis, psoriasis, and hypersensitivity disorders.
 CC This is the amino acid sequence of ovine interferon-tau.
 CC
 XX
 SO Sequence 172 AA;
 QY Query Match 100.0%; Score 907; DB 8; Length 172;
 Best Local Similarity 100.0%; Pred. No. 1e-92;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CYLSRKLMLDARENKLLDRNMRUSPHSCLQDRKDFGLPQEVNEDGDLQKQDAFPVLYEM 60
 |||

DB 1 CYLSRKLMLDARENKLLDRNMRUSPHSCLQDRKDFGLPQEVNEDGDLQKQDAFPVLYEM 60
 QY 61 LQGSFNLFTYTHSSAAMDITLLLEQLCTGLQQQLDHLDTCRGVWGEEDSELGNDPIVTV 120
 DB 61 LQGSFNLFTYTHSSAAMDITLLLEQLCTGLQQQLDHLDTCRGVWGEEDSELGNDPIVTV 120

QY 121 KKYFGIYDYLQEKGYSDCAMEIIVVENMRALTIVSTTLQKRLTKMGDLNSP 172
 DB 121 KKYFGIYDYLQEKGYSDCAMEIIVVENMRALTIVSTTLQKRLTKMGDLNSP 172

RESULT 9
 AAR04540
 ID AAR04540 standard; protein; 195 AA.
 AC AAR04540;
 XX
 DT 25-MAR-2003 (revised)
 DT 17-SEP-1990 (first entry)
 XX
 DE Ovine trophoblast protein-1 (OTP-1).
 KW Bovine trophoblast protein-1; bTP-1; fertility; ds.
 KW
 OS Sus scrofa.
 XX
 PN EP367063-A.
 XX
 PD 09-MAY-1990.
 XX
 PE 23-OCT-1989; 89EP-00119642.
 XX
 PR 26-OCT-1988; 88US-00262870.
 XX
 PA (UMOR) UNIV MISSOURI.
 XX
 PI Roberts MR, Imakawa K;
 XX
 DR WPI; 1990-141062/19.
 DR N-PSDB; AAO04289.
 XX
 PT Recombinant bovine trophoblast protein-1 - used for enhancing fertility
 PT or treating viral diseases in mammal, esp. cattle.
 XX
 PS Disclosure; Page ?; 27pp; English.
 XX
 CC The bTP-1 produced from the gene may be used to promote fertility or
 CC treat viral disease in cattle. The gene may also be used to provide
 CC transgenic animals with enhanced fertility, or in prophylactic and
 CC therapeutic treatment of other mammals. (Updated on 25-MAR-2003 to
 CC correct PA field.)
 XX
 SO Sequence 195 AA;
 QY Query Match 100.0%; Score 907; DB 2; Length 195;
 Best Local Similarity 100.0%; Pred. No. 1.2e-92;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CYLSRKLMLDARENKLLDRNMRUSPHSCLQDRKDFGLPQEVNEDGDLQKQDAFPVLYEM 60
 |||

QY 24 CYLSRKLMLDARENKLLDRNMRUSPHSCLQDRKDFGLPQEVNEDGDLQKQDAFPVLYEM 83
 DB 24 LQGSFNLFTYTHSSAAMDITLLLEQLCTGLQQQLDHLDTCRGVWGEEDSELGNDPIVTV 143
 QY 61 LQGSFNLFTYTHSSAAMDITLLLEQLCTGLQQQLDHLDTCRGVWGEEDSELGNDPIVTV 120
 DB 61 LQGSFNLFTYTHSSAAMDITLLLEQLCTGLQQQLDHLDTCRGVWGEEDSELGNDPIVTV 143

QY 121 KKYFGIYDYLQEKGYSDCAMEIIVVENMRALTIVSTTLQKRLTKMGDLNSP 172
 DB 144 KKYFGIYDYLQEKGYSDCAMEIIVVENMRALTIVSTTLQKRLTKMGDLNSP 195

RESULT 10
 AAR09294

```
ID AAR09294 standard; protein; 172 AA.
XX
AC AAR09294;
XX
XX 25-MAR-2003 (revised)
DT 22-JAN-1991 (first entry)
XX
DE Ovine trophoblast protein-1.
XX
XX Interferon; tumour; virus; retrovirus; cancer; AIDS.
XX
OS Ovis aries.
XX
XX
FH Key Location/Qualifiers
FT Peptide 18..53
FT Peptide 68..76
FT Peptide 88..114
FT Peptide 130..138
FT Peptide 159..172
XX
XX WO9009806-A.
XX
XX 07-SEP-1990.
XX
XX 02-MAR-1989; 89US-00318050.
XX
XX 02-MAR-1989; 89US-00318050.
XX
XX (UYFL ) UNIV FLORIDA.
XX
XX Bazer FW, Johnson HM;
XX
XX WPI; 1990-290161/38.
XX
XX Non-cytotoxic inhibition of viruses and tumours - using conceptus-derived
PT ovine trophoblast protein-1.
XX
XX PS Disclosure; Fig 1; 20pp; English.
XX
XX CC This conceptus-derived ovine trophoblast protein-1 (OTF-1) is used in a
CC compsn. for inhibiting tumour growth or viral replic- action. It is an
CC interferon and exerts its inhibitory effect on viruses , retroviruses and
CC tumours without harming the cells of the host animal. Its fragments
CC (indicated in features), or immunologically equivalent variants can also
CC be used. (Updated on 25-MAR-2003 to correct PA field.)
XX
XX SQ Sequence 172 AA;
XX
XX Query Match 99.8%; Score 905; DB 2; Length 172;
XX Best Local Similarity 99.4%; Pred. No. 1.7e-92;
XX Matches 171; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CYLSRKMLDARENKILDRNRLSPHSCLODRKDFGLPQEMVEGDQLQKQAPPLYEM 60
XX DB 1 CYLSRKMLDARENKILDRNRLSPHSCLODRKDFGLPQEMVEGDQLQKQAPPLYEM 60
XX
XX QY 61 LQGSFNLPTTEHSSAAMDITLLEQLCTGLQOQLDHLPTCRGQVWGBEBSSELGNDPIYTV 120
XX DB 61 LQGSFNLPTTEHSSAAMDITLLEQLCTGLQOQLDHLPTCRGQVWGBEBSSELGNDPIYTV 120
XX
XX QY 121 KKYFGIYDYLOEKGYSDCAMEIYVEMMRALTVSTTLQKRLTVMGDLNSP 172
XX DB 121 KKYFGIYDYLOEKGYSDCAMEIYVEMMRALTVSTTLQKRLTVMGDLNSP 172
XX
XX
XX RESULT 11
XX ID ADM79195 standard; protein; 172 AA.
XX
XX AC ADM79195;
XX
XX DT 15-JUL-2004 (first entry)
XX
```

```
DE Interferon tau protein.
XX
XX oral administration; interferon; IFN; mature interferon tau.
XX
XX OS Unidentified.
XX
XX PN WO2004032863-A2.
XX
XX 22-APR-2004.
XX
XX PD 08-OCT-2003; 2003WO-US031999.
XX
XX PF 09-OCT-2002; 2002US-0417292P.
XX
XX PR (PEPG-) PEPGEN CORP.
XX
XX PA Manning MC, Nayar R;
XX
XX PI Manning MC, Nayar R;
XX
XX DR WPI; 2004-340799/31.
XX
XX FT A composition for oral administration of an interferon (IFN) comprises an
XX PT IFN and a species that stabilizes the IFN in an active form by
XX interaction between the interferon and the species.
XX
XX PS Disclosure; Fig 1A; 52pp; English.
XX
XX CC The present invention describes a composition for the oral administration
XX of an interferon (IFN) comprising an IFN and a species that stabilizes
XX the IFN in an active form by interaction between the IFN and the species.
XX CC Also described: (1) preparing a protein for oral administration,
XX comprising formulating the protein with a species that stabilizes the
XX protein in an active form by binding interaction between the protein and
XX the species; therefore the formulating results in a composition for oral
XX administration; and (2) selecting a dosage form composition for a protein
XX that achieves protein stabilisation for biological activity upon in vivo
XX administration, comprising selecting a protein for formulation, preparing
XX solutions of the selected protein or polypeptide in different buffers at
XX different pH values, and measuring the effect of the buffer on the
XX protein's tertiary structure, where the measuring identifies buffers that
XX result retention of the protein's tertiary structure. The composition and
XX methods are useful for preparing oral dosage forms for administration of
XX proteins and polypeptides. The present sequence represents an interferon
XX tau amino acid sequence, which is used in the exemplification of the
XX present invention.
XX
XX SQ Sequence 172 AA;
XX
XX Query Match 99.8%; Score 905; DB 8; Length 172;
XX Best Local Similarity 99.4%; Pred. No. 1.7e-92;
XX Matches 171; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CYLSRKMLDARENKILDRNRLSPHSCLODRKDFGLPQEMVEGDQLQKQAPPLYEM 60
XX DB 1 CYLSRKMLDARENKILDRNRLSPHSCLODRKDFGLPQEMVEGDQLQKQAPPLYEM 60
XX
XX QY 61 LQGSFNLPTTEHSSAAMDITLLEQLCTGLQOQLDHLPTCRGQVWGBEBSSELGNDPIYTV 120
XX DB 61 LQGSFNLPTTEHSSAAMDITLLEQLCTGLQOQLDHLPTCRGQVWGBEBSSELGNDPIYTV 120
XX
XX QY 121 KKYFGIYDYLOEKGYSDCAMEIYVEMMRALTVSTTLQKRLTVMGDLNSP 172
XX DB 121 KKYFGIYDYLOEKGYSDCAMEIYVEMMRALTVSTTLQKRLTVMGDLNSP 172
XX
XX
XX RESULT 12
XX ID AAR24942 standard; protein; 195 AA.
XX
XX AC AAR24942;
XX
XX DT 25-MAR-2003 (revised)
XX DT 03-JAN-1992 (first entry)
XX
```

```

DE Sequence of ovien trophoblastin variant Xa.
XX Antiviral; antiinflammatory; antitumour; immunomodulator; immunogen;
KW trophoblastin; antitubercytic agent.
XX
XX Ammotragus lervia.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= signal
XX
XX MO9209691-A1.
XX
XX 11-JUN-1992.
XX
XX 29-NOV-1991; 91WO-FR000953.
XX
XX 29-NOV-1990; 90FR-00014945.
XX 29-NOV-1990; 90FR-00014946.
XX (INRG ) INRA INST NAT RECH AGRONOMIQUE.
XX
XX Martal J, Degryse E, Gaye P, Charlier M, Charpigny G, Reinaud P;
XX Chaouat G;
XX
XX WPI; 1992-217070/26.
XX
XX New type I interferon variants with added N-terminal dipeptide - include
XX expression cassettes providing high yield in yeast, esp. trophoblast
XX derivative, with e.g. anti-tubercytic activity.
XX
XX Claim 7; Page 30; 53pp; French.
XX
XX The DNA sequence encoding the precursor of ovine trophoblastin was
XX disclosed in PCT WO 89/08706 (see AAR24941). AAR24942-R24945 are isoforms
XX of trophoblastin. They have anti-tubercytic activity and are used to
XX improve survival of transplanted embryos, as a reagent for detecting
XX viability of embryos at an early stage of its development; and to improve
XX the fertility of livestock. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 195 AA;
SQ
Query Match 99.7%; Score 904; DB 2; Length 195;
Best Local Similarity 99.4%; Pred. No. 2.7e-92;
Matches 171; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 CYLSRKMLDARENKLLDRNMRSLPHSCLODRKDFGLPOEMVEGDLOKQOAPFVLYEM 60
Db 24 CYLSRKMLDARENKLLDRNMRSLPHSCLODRKDFGLPOEMVEGDLOKQOAPFVLYEM 83
OY 61 LQGSFNLFTYHSSAAMDITLLLEQCTGLQOQLDHLDTCRGOVMEEDSELGNDPIVTV 120
Db 84 LQGSFNLFTYHSSAAMDITLLDQCTGLQOQLDHLDTCRGOVMEEDSELGNDPIVTV 143
OY 121 KKYFQGIYDYLOEKGYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 172
Db 144 KKYFQGIYDYLOEKGYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 195
RESULT 13
AAB31457
ID AAB31457 standard; protein; 172 AA.
XX
XX AAB31457;
XX
XX 20-APR-2001 (first entry)
XX
XX Amino acid sequence of an ovine interferon-tau 1mod polypeptide.
XX
XX Interferon-tau; IFN-tau; cancer; tumour growth; viral disease;
XX autoimmune disease; multiple sclerosis; adenocarcinoma; breast cancer;
XX prostate cancer; glioblastoma; melanoma; myeloma; lymphoma; leukaemia;
XX lung cancer; skin cancer; bladder cancer; kidney cancer; brain cancer;

```

```

KW ovarian cancer; pancreatic cancer; uterine cancer; bone cancer;
KW colorectal cancer; cervical cancer; neuroectodermal cancer; psoriasis;
KW monoclonal gammopathy; dysplasia; diabetes mellitus;
KW rheumatoid arthritis; lupus erythematosus.
XX
XX Ovis sp.
XX
XX MO200078266-A2.
XX
XX 28-DEC-2000.
XX
XX 22-JUN-2000; 2000MO-IB001080.
XX
XX 22-JUN-1999; 99US-0140411P.
XX (UYMA-) UNIV MARYLAND BALTIMORE.
XX
XX Pontzer CH, Shortz LH, Clark CD;
XX
XX WPI; 2001-071357/08.
XX N-PSDB; AAF24827.
XX
XX Producing recombinant interferon tau analog proteins with improved
XX properties, useful for treating cancers, autoimmune diseases and viral
XX infections.
XX
XX Claim 5; Page 59-60; 70pp; English.
XX
XX The present sequence represents an ovine interferon-tau 1mod polypeptide.
XX The specification describes a method of making recombinant interferon
XX (IFN)-tau proteins, which differ from wild-type IFN-tau by amino acid
XX substitutions near the amino terminus of the molecule. The mutated IFN-
XX tau proteins have improved biological activity, low toxicity, retain the
XX same or slightly reduced antiviral activity compared with interferon
XX alpha, and have enhanced antiproliferative activity compared to wild-type
XX IFN-tau. The method is used for producing IFN-tau proteins with improved
XX biological activities and properties. These IFN-tau may be administered
XX to treat cancers and decrease tumour growth, treat viral diseases, treat
XX autoimmune diseases and treat multiple sclerosis. The cancer or tumour is
XX selected from the group comprising human adenocarcinoma, breast cancer,
XX prostate cancer, glioblastomas, melanomas, myelomas, lymphomas,
XX leukaemia, lung cancer, skin cancer, bladder cancer, kidney cancer, brain
XX cancer, ovarian cancer, pancreatic cancer, uterine cancer, bone cancer,
XX colorectal cancer, cervical cancer and neuroectodermal cancer, monoclonal
XX gammopathies and cervical and oral dysplasia. The autoimmune disease is
XX selected from Type I diabetes mellitus, rheumatoid arthritis, lupus
XX erythematosus and/or psoriasis. The viral infection is an RNA virus, a
XX human immuno deficiency virus (HIV) or hepatitis C virus
XX
XX Sequence 172 AA;
SQ
Query Match 99.2%; Score 900; DB 4; Length 172;
Best Local Similarity 99.4%; Pred. No. 6.3e-92;
Matches 171; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CYLSRKMLDARENKLLDRNMRSLPHSCLODRKDFGLPOEMVEGDLOKQOAPFVLYEM 60
Db 1 CYLSRKMLDARENKLLDRNMRSLPHSCLODRKDFGLPOEMVEGDLOKQOAPFVLYEM 60
OY 61 LQGSFNLFTYHSSAAMDITLLLEQCTGLQOQLDHLDTCRGOVMEEDSELGNDPIVTV 120
Db 61 LQGSFNLFTYHSSAAMDITLLLEQCTGLQOQLDHLDTCRGOVMEEDSELGNDPIVTV 120
OY 121 KKYFQGIYDYLOEKGYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 172
Db 121 KKYFQGIYDYLOEKGYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 172
RESULT 14
AA021461
ID AA021461 standard; protein; 172 AA.
XX
XX AA021461;
AC

```


XX 15-AUG-2002 (first entry)
 DT
 XX
 XX Ovine interferon-tau (OvIFN-tau) protein.
 DE
 XX
 XX Artificial ovine interferon-tau; OvIFN-tau; optimizing; biased codon;
 KM high yield production.
 XX
 XX Ovis aries.
 OS
 XX Synthetic.
 XX
 XX MO200231178-A1.
 PN
 XX 18-APR-2002.
 PD
 XX 12-OCT-2001; 2001MO-US031862.
 PF
 XX 12-OCT-2000; 2000US-0239746P.
 PR
 XX 12-OCT-2000; 2000US-0239746P.
 PA
 XX (UABR-) UAB RES FOUND.
 PI
 XX Krishna R, Rodriguez E, Johnson H;
 XX
 XX WPI; 2002-426289/45.
 DR
 XX N-PSDB; AAL38060.
 DT
 XX
 XX New artificial ovine interferon-tau gene, useful for high protein
 PT production, constructed by reducing repetitive and palindromic sequences,
 PT lowering overall guanine and cytosine content and optimizing gene
 PT sequence.
 PS
 XX Disclosure; Fig 1A; 71pp; English.
 XX
 XX The invention relates to an artificial ovine interferon-tau (OvIFN-tau)
 CC gene designed for high yield protein production in yeast, and constructed
 CC by reducing repetitive sequences, lowering overall G+C content, reducing
 CC or eliminating palindromic sequences, and optimizing the sequence of
 CC OvIFN-tau, using the biased codon usage in the yeast. The expression
 CC vector of the invention is useful for high yield production of OvIFN-tau
 CC in the yeast of *Pichia*, preferably *P. pastoris* X33 or *P. pastoris* GS115,
 CC by transforming the yeast with the expression vector, inducing protein
 CC expression with methanol, culturing the yeast in defined culture
 CC conditions such as shake flask or fermenter, and purifying the protein
 CC from culture media. This sequence represents the ovine interferon-tau
 CC (OvIFN-tau) protein of the invention
 CC
 XX
 SO Sequence 172 AA;
 Query Match 99.2%; Score 900; DB 5; Length 172;
 Best Local Similarity 99.4%; Pred. No. 6.3e-92;
 Matches 171; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CYLSRKMLDARENKLLDRNNRSLPHSCLODRKDFGLPQEMVGGDQLQKQAPFVLYEM 60
 DB 1 CYLSRKMLDARENKLLDRNNRSLPHSCLODRKDFGLPQEMVGGDQLQKQAPFVLYEM 60
 QY 61 LOGSFNLFTYTHSSAAMDITLLLEQLCTGLQOQDLHDLTCRGQVWGEEDSELGNDPIVTV 120
 DB 61 LOGSFNLFTYTHSSAAMDITLLLEQLCTGLQOQDLHDLTCRGQVWGEEDSELGNDPIVTV 120
 QY 121 KKYFQGIYDYLQEKGYSDCAWEIVRVEEMRALTVSTTLQKRLTGMGDLNSP 172
 DB 121 KKYFQGIYDYLQEKGYSDCAWEIVRVEEMRALTVSTTLQKRLTGMGDLNSP 172
 RESULT 15
 ID ABB07589 standard; protein; 172 AA.
 AC ABB07589;
 XX
 XX 08-MAY-2002 (first entry)
 DT
 XX

DE Recombinant ovine interferon-tau protein.
 XX
 XX Hepatitis C virus; HCV infection; ovine; interferon-tau; OvIFN-tau; OAS;
 KM 2',5'-oligoadenylate synthetase; virucide; hepatotropic; IFN-tau.
 XX
 XX Ovis aries.
 OS
 XX WO200206343-A2.
 PN
 XX 24-JAN-2002.
 PD
 XX 19-JUL-2001; 2001MO-US022976.
 PF
 XX 19-JUL-2000; 2000US-0219128P.
 PR 17-OCT-2000; 2000JP-00317160.
 PA
 XX (PEPG-) PEPGEN CORP.
 PI
 XX Sokawa Y, Liu C;
 XX
 XX WPI; 2002-179784/23.
 DR
 XX N-PSDB; ABA94937.
 DT
 XX
 XX Oral-delivery composition for treating conditions relating to hepatitis
 PT caused by hepatitis C virus, comprises ovine interferon-tau which
 PT stimulates bloodstream levels of 2',5'-oligoadenylate synthetase.
 PS
 XX Example 1; Page 33; 33pp; English.
 XX
 XX The invention provides an oral-delivery composition for use in treating
 CC hepatitis C virus (HCV) in a HCV-infected patient. The composition
 CC comprises ovine interferon-tau (OvIFN-tau), in a dosage effective to
 CC stimulate bloodstream levels of 2',5'-oligoadenylate synthetase (OAS).
 CC The OvIFN-tau synthesizes OAS which degrades viral mRNA. A method is also
 CC provided for monitoring the treatment of HCV by oral administration of
 CC OvIFN-tau, by measuring the blood levels of OAS prior to and after such
 CC oral administration, and if necessary, adjusting the dose of IFN-tau
 CC until a measurable increase in blood OAS level, relative to the level
 CC observed prior to administration. The composition is useful for treating
 CC hepatitis caused by HCV and the method is useful for monitoring treatment
 CC of HCV by oral administration of OvIFN-tau. The present sequence
 CC represents a recombinant ovine interferon-tau protein
 CC
 XX
 SO Sequence 172 AA;
 Query Match 99.1%; Score 899; DB 5; Length 172;
 Best Local Similarity 98.8%; Pred. No. 8.1e-92;
 Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CYLSRKMLDARENKLLDRNNRSLPHSCLODRKDFGLPQEMVGGDQLQKQAPFVLYEM 60
 DB 1 CYLSRKMLDARENKLLDRNNRSLPHSCLODRKDFGLPQEMVGGDQLQKQAPFVLYEM 60
 QY 61 LOGSFNLFTYTHSSAAMDITLLLEQLCTGLQOQDLHDLTCRGQVWGEEDSELGNDPIVTV 120
 DB 61 LOGSFNLFTYTHSSAAMDITLLLEQLCTGLQOQDLHDLTCRGQVWGEEDSELGNDPIVTV 120
 QY 121 KKYFQGIYDYLQEKGYSDCAWEIVRVEEMRALTVSTTLQKRLTGMGDLNSP 172
 DB 121 KKYFQGIYDYLQEKGYSDCAWEIVRVEEMRALTVSTTLQKRLTGMGDLNSP 172
 RESULT 16
 ID ADM79178 standard; protein; 172 AA.
 AC ADM79178;
 XX
 XX 15-JUL-2004 (first entry)
 DT
 XX Mature ovine interferon tau variant protein SEQ ID NO:2.
 DE
 XX oral administration; interferon; IFN; ovine; mature interferon tau;
 KM

KW variant.
 OS Ovis aries.
 OS Synthetic.
 XX MO2004032863-A2.
 XX
 PD 22-APR-2004.
 XX
 XX 08-OCT-2003; 2003WO-US031999.
 XX
 XX 09-OCT-2002; 2002US-0417292P.
 XX
 PA (PERG-) PERGEN CORP.
 XX
 PI Manning MC, Nayar R;
 XX
 DR WPI, 2004-340799/31.
 XX
 PT A composition for oral administration of an interferon (IFN) comprises an
 FT IFN and a species that stabilizes the IFN in an active form by
 PT interaction between the interferon and the species.
 XX
 PS Example; SEQ ID NO 2; 52bp; English.
 XX
 CC The present invention describes a composition for the oral administration
 CC of an interferon (IFN) comprising an IFN and a species that stabilizes
 CC the IFN in an active form by interaction between the IFN and the species.
 CC Also described: (1) preparing a protein for oral administration,
 CC comprising formulating the protein with a species that stabilizes the
 CC protein in an active form by binding interaction between the protein and
 CC the species; therefore the formulating results in a composition for oral
 CC administration; and (2) selecting a dosage form composition for a protein
 CC that achieves protein stabilization for biological activity upon in vivo
 CC administration, comprising selecting a protein for formulation, preparing
 CC solutions of the selected protein or polypeptide in different buffers at
 CC different pH values, and measuring the effect of the buffer on the
 CC protein's tertiary structure, where the measuring identifies buffers that
 CC result retention of the protein's tertiary structure. The composition and
 CC methods are useful for preparing oral dosage forms for administration of
 CC proteins and polypeptides. The present sequence represents a mature ovine
 CC interferon tau variant amino acid sequence where positions 5 and 6 have
 CC been modified, which is used in an example from the present invention.
 XX
 SQ Sequence 172 AA;
 Query Match 99.1%; Score 899; DB 8; Length 172;
 Best Local Similarity 98.8%; Pred. No. 8.1e-92;
 Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CYLSRKMLDARENLKLLDRNNRSLSPHSCLDRKDFGLPOEWEBCDQLOKQAPPVLYEM 60
 DB 1 CYLSERMLDARENLKLLDRNNRSLSPHSCLDRKDFGLPOEWEBCDQLOKQAPPVLYEM 60
 QY 61 LQGSFNLFTYEHSSAAMDITLLBOLCTGLQOQDLHLDTCRQGVWGEBSDELGNNDPIVTV 120
 DB 61 LQGSFNLFTYEHSSAAMDITLLBOLCTGLQOQDLHLDTCRQGVWGEBSDELGNNDPIVTV 120
 QY 121 KKYFGIYDYLOEKGYSDCAMEIVVEMRALTVSTTLQKRLTKGGLNSP 172
 DB 121 KKYFGIYDYLOEKGYSDCAMEIVVEMRALTVSTTLQKRLTKGGLNSP 172
 RESULT 17
 ADS13614
 ID ADS13614 standard; protein; 172 AA.
 XX
 AC ADS13614;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Recombinant sheep interferon tau seqid 3.
 XX

KW immunosuppressive; cytostatic; virucide; neuroprotective; antidiabetic;
 KW muscular; antiinflammatory; antirheumatic; antiarthritic; antisthmatic;
 KW dermatological; vaccinia; interferon tau; 2',5'-oligoadenylate synthetase;
 KW OAS; autoimmune condition; cancer; viral infection; multiple sclerosis;
 KW hepatitis C infection; diabetes mellitus; systemic lupus erythematosus;
 KW amyotrophic lateral sclerosis; Crohn's disease; rheumatoid arthritis;
 KW asthma; uveitis; psoriasis; hypersensitivity disorder; sheep.
 XX
 XX Ovis aries.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 5 /note= "Wild type Arg substituted by Glu"
 FT FT
 FT Misc-difference 6 /note= "Wild type Lys substituted by Arg"
 FT FT
 XX US2004191217-A1.
 XX
 XX 30-SEP-2004.
 PD
 PD 21-NOV-2003; 2003US-00719472.
 XX
 XX 19-JUN-2000; 2000US-0219128P.
 PR 19-JUN-2001; 2001US-00310406.
 PR 16-JAN-2002; 2002US-0349658P.
 PR 16-JAN-2003; 2003US-00346269.
 PR 31-OCT-2003; 2003US-00698927.
 XX
 PA (SOKA/) SOKAWA Y.
 PA (LTUC/) LTU C.
 XX
 PI Sotawa Y, Liu C;
 XX
 DR WPI; 2004-698654/68.
 DR N-PSDB; ADS13615.
 XX
 XX Treating a condition in a subject, e.g. autoimmune condition, cancer or
 FT viral infection, comprises orally administering interferon-tau to the
 FT intestinal tract to increase the blood 2',5'-oligoadenylate synthetase
 FT level.
 PS Claim 2; SEQ ID NO 3; 38bp; English.
 XX
 XX The invention describes a method of treating a condition in a human
 CC subject responsive to interferon tau therapy comprising orally
 CC administering interferon-tau to the intestinal tract of the subject to
 CC produce an initial measurable increase in the subject's blood 2',5'-
 CC oligoadenylate synthetase (OAS) level, relative to the blood OAS level in
 CC the subject in the absence of interferon-tau administration. The method
 CC is useful for treating an autoimmune condition, cancer, or a viral
 CC infection. The method is particularly useful for treating multiple
 CC sclerosis or hepatitis C infection, diabetes mellitus, systemic lupus
 CC erythematosus, amyotrophic lateral sclerosis, Crohn's disease, rheumatoid
 CC arthritis, asthma, uveitis, psoriasis, and hypersensitivity disorders.
 CC This is the amino acid sequence of recombinant ovine interferon-tau in
 CC which the residues at positions 5 and 6 have been altered to Glu and Arg
 CC relative to the wild type Arg and Lys.
 XX
 SQ Sequence 172 AA;
 Query Match 99.1%; Score 899; DB 8; Length 172;
 Best Local Similarity 98.8%; Pred. No. 8.1e-92;
 Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CYLSRKMLDARENLKLLDRNNRSLSPHSCLDRKDFGLPOEWEBCDQLOKQAPPVLYEM 60
 DB 1 CYLSERMLDARENLKLLDRNNRSLSPHSCLDRKDFGLPOEWEBCDQLOKQAPPVLYEM 60
 QY 61 LQGSFNLFTYEHSSAAMDITLLBOLCTGLQOQDLHLDTCRQGVWGEBSDELGNNDPIVTV 120
 DB 61 LQGSFNLFTYEHSSAAMDITLLBOLCTGLQOQDLHLDTCRQGVWGEBSDELGNNDPIVTV 120

OY 121 KKYFGIYDYLOEKGYSDCAMEIYRVEMRALTIVSTTLQKRLTKMGDLNSP 172
DB 121 KKYFGIYDYLOEKGYSDCAMEIYRVEMRALTIVSTTLQKRLTKMGDLNSP 172

RESULT 18

AAB31462 standard; protein; 172 AA.

AC AAB31462;

DT 20-APR-2001 (first entry)

DE An ovine interferon-tau lmod polypeptide with mutation L241.

XX Interferon-tau; IFN-tau; cancer; tumour growth; viral disease;
KW autoimmune disease; multiple sclerosis; adenocarcinoma; breast cancer;
KW prostate cancer; glioblastoma; melanoma; myeloma; lymphoma; leukaemia;
KW lung cancer; skin cancer; bladder cancer; kidney cancer; brain cancer;
KW ovarian cancer; pancreatic cancer; uterine cancer; bone cancer;
KW colorectal cancer; cervical cancer; neuroectodermal cancer; psoriasis;
KW monoclonal gammopathy; dysplasia; diabetes mellitus;
KW rheumatoid arthritis; lupus erythematosus.

OS Synthetic.

OS Ovis sp.

PN WO200078266-A2.

PD 28-DEC-2000.

PF 22-JUN-2000; 2000WO-IB001080.

PR 22-JUN-1999; 99US-0140411P.

PA (UYMA-) UNIV MARYLAND BALTIMORE.

PI Pontzer CH, Shorts LH, Clark CD;

DR WPI; 2001-071357/08.

DR N-PSDB; AAF24831.

PT Producing recombinant interferon tau analog proteins with improved
PT properties, useful for treating cancers, autoimmune diseases and viral
PT infections.

PS Claim 15; Page 64; 70pp; English.

XX The present sequence represents a mutated ovine interferon-tau lmod
CC polypeptide, which was made using the method of the invention. The
CC specification describes a method of making recombinant interferon (IFN)-
CC tau proteins, which differ from wild-type IFN-tau by amino acid
CC substitutions near the amino terminus of the molecule. The mutated IFN-
CC tau proteins have improved biological activity, low toxicity, retain the
CC same or slightly enhanced antiviral activity compared with interferon
CC alpha, and have enhanced antiproliferative activity compared to wild-type
CC IFN-tau. The method is used for producing IFN-tau proteins with improved
CC biological activities and properties. These IFN-tau may be administered
CC to treat cancers and decrease tumour growth. Treat viral diseases, treat
CC autoimmune diseases and treat multiple sclerosis. The cancer or tumour is
CC selected from the group comprising human adenocarcinoma, breast cancer,
CC prostate cancer, glioblastomas, melanomas, myelomas, lymphomas,
CC leukemia, lung cancer, skin cancer, bladder cancer, kidney cancer, brain
CC cancer, ovarian cancer, pancreatic cancer, uterine cancer, bone cancer,
CC colorectal cancer, cervical cancer and neuroectodermal cancer, monoclonal
CC gammopathies and cervical and oral dysplasia. The autoimmune disease is
CC erythematous and/or psoriasis. The viral infection is an RNA virus, a
CC human immuno deficiency virus (HIV) or hepatitis C virus
XX Sequence 172 AA;

Query Match 99.0%; Score 898; DB 4; Length 172;

Best Local Similarity 98.8%; Pred. No. 1e-91;
Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CYSRKIMLDARENLKILDRMNRISPHSCIQDRKDFGLPQEWVGDLQKQDAFPVLYEM 60

DB 1 CYSRKIMLDARENLKILDRMNRISPHSCIQDRKDFGLPQEWVGDLQKQDAFPVLYEM 60

OY 61 LQOSFNLPTHESSAANDTTLLEOLCTGLQOQDLHLDTCGQVWGEEDSELGNMPTVTV 120

DB 61 LQOSFNLPTHESSAANDTTLLEOLCTGLQOQDLHLDTCGQVWGEEDSELGNMPTVTV 120

OY 121 KKYFGIYDYLOEKGYSDCAMEIYRVEMRALTIVSTTLQKRLTKMGDLNSP 172

DB 121 KKYFGIYDYLOEKGYSDCAMEIYRVEMRALTIVSTTLQKRLTKMGDLNSP 172

RESULT 19

AAR24941 standard; protein; 195 AA.

AC AAR24941;

DT 25-MAR-2003 (revised)

DT 03-JAN-1992 (first entry)

DE Sequence of ovine trophoblastin.

XX Antiviral; antiinflammatory; antitumour; immunomodulator; immunogen;

KW trophoblastin; antileukolytic agent.

OS Ammotragus lervia.

EH Key Location/Qualifiers

FT 1..23 /label= signal

PN WO9209691-A1.

PD 11-JUN-1992.

PF 29-NOV-1991; 91WO-FR000953.

PR 29-NOV-1990; 90FR-00014945.

PR 29-NOV-1990; 90FR-00014946.

PA (INRG) INRA INST NAT RECH AGRONOMICUE.

PI Martal J, Degryse E, Gaye P, Charlier M, Charpigny G, Renaud P,

PI Chaouat G;

DR WPI; 1992-217070/26.

XX New type I interferon variants with added N-terminal dipeptide - include
PT expression cassettes providing high yield in yeast, esp. trophoblast
PT derive. with e.g. anti-leukolytic activity.

PS Disclosure; Fig 1; 53pp; French.

XX The DNA sequence encoding the precursor of ovine trophoblastin was
CC disclosed in PCT WO 89/08706 (see AAR24941). AAR24942-R24945 are isoforms
CC of trophoblastin. They have anti-leukolytic activity and are used to
CC improve survival of transplanted embryos; as a reagent for detecting
CC viability of embryos at an early stage of its development; and to improve
CC the fertility of livestock. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 195 AA;

Query Match 98.9%; Score 897; DB 2; Length 195;
Best Local Similarity 98.3%; Pred. No. 1.6e-91;
Matches 169; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 CYSRKIMLDARENLKILDRMNRISPHSCIQDRKDFGLPQEWVGDLQKQDAFPVLYEM 60
||||:|||||

```

Db      24  CYLSORLMLDARENKLDLRNRLSPHSCLODRKDFGLPQEWVEGDQLQKQAFPVLYEM 83
Oy      61  LQGSFNLFTYTESHAAMDITLLLEQLCTGILQOQLDHLDTCRGVWGEEDSELGNMPTIVTV 120
Db      84  LQGSFNLFTYTESHAAMDITLLDQLCTGILQOQLDHLDTCRGVWGEEDSELGNMPTIVTV 143
Oy      121 KKYFGIYDYLOEKGYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 172
Db      144 KKYFGIYDYLOEKGYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 195

RESULT 20
AAR24945
ID      AAR24945 standard; protein; 195 AA.
AC      AAR24945;
XX
XX      25-MAR-2003 (revised)
DT      03-JAN-1992 (first entry)
XX
XX      Sequence of ovine trophoblastin variant Xd.
DE
XX      Antiviral; antiinflammatory; antitumour; immunomodulator; immunogen;
KW      trophoblastin; antileukolytic agent.
XX
XX      Ammotreagus lervia.
OS
XX
XX      Key      Location/Qualifiers
FH      Peptide 1..23
FT
FT      /label= signal
XX
XX      WO9209691-A1.
XX
XX      11-JUN-1992.
XX
XX      29-NOV-1991; 91WO-FR000953.
XX
XX      29-NOV-1990; 90FR-00014945.
XX      29-NOV-1990; 90FR-00014946.
XX
XX      (INRG ) INRA INST NAT RECH AGRONOMIQUE.
XX
XX      Martal J, Degryse E, Gage P, Charlier M, Charpigny G, Reinaud P;
PI      Chaouat G;
XX
XX      WPI; 1992-217070/26.
XX
XX      New type I interferon variants with added N-terminal dipeptide - include
PT      expression cassettes providing high yield in yeast, esp. trophoblast
PT      derivative, with e.g. anti-leukolytic activity.
XX
XX      Claim 7; Page 30; 53pp; French.
XX
XX      The DNA sequence encoding the precursor of ovine trophoblastin was
CC      disclosed in PCT WO 89/08706 (see AAR24941). AAR24942-R24945 are isoforms
CC      of trophoblastin. They have anti-leukolytic activity and are used to
CC      improve survival of transplanted embryos; as a reagent for detecting
CC      viability of embryos at an early stage of its development; and to improve
CC      the fertility of livestock. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX      Sequence 195 AA:
SQ
Query Match 98.9%; Score 897; DB 2; Length 195;
Best Local Similarity 98.3%; Pred. No. 1,6e-91;
Matches 169; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      121 KKYFGIYDYLOEKGYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 172
Db      144 KKYFGIYDYLOEKGYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 195

RESULT 21
AAB31468
ID      AAB31468 standard; protein; 172 AA.
AC      AAB31468;
XX
XX      20-APR-2001 (first entry)
DT
XX
XX      An ovine interferon-tau Imod polypeptide with mutation R20Q.
DE
XX
XX      Interferon-tau; IFN-tau; cancer; tumour growth; viral disease;
KW      autoimmune disease; multiple sclerosis; adenocarcinoma; breast cancer;
KW      prostate cancer; glioblastoma; melanoma; myeloma; lymphoma; leukaemia;
KW      lung cancer; skin cancer; bladder cancer; kidney cancer; brain cancer;
KW      ovarian cancer; pancreatic cancer; uterine cancer; bone cancer;
KW      colorectal cancer; cervical cancer; neuroectodermal cancer; psoriasis;
KW      monoclonal gammopathy; dysplasia; diabetes mellitus;
KW      rheumatoid arthritis; lupus erythematosus.
XX
XX      Synthetic.
OS
XX      Ovis sp.
XX
XX      WO200078266-A2.
XX
XX      28-DEC-2000.
XX
XX      22-JUN-2000; 2000WO-IB001080.
XX
XX      22-JUN-1999; 99US-0140411P.
XX
XX      (UTMA-) UNIV MARYLAND BALTIMORE.
XX
XX      Pontzer CH, Shorts LH, Clark CD;
PI
XX
XX      WPI; 2001-071357/08.
XX
XX      Producing recombinant interferon tau analog proteins with improved
PT      properties, useful for treating cancers, autoimmune diseases and viral
PT      infections.
XX
XX      Claim 15; Page 69-70; 70pp; English.
XX
XX      The present sequence represents a mutated ovine interferon-tau Imod
CC      polypeptide, which was made using the method of the invention. The
CC      specification describes a method of making recombinant interferon (IFN)-
CC      tau proteins, which differ from wild-type IFN-tau by amino acid
CC      substitutions near the amino terminus of the molecule. The mutated IFN-
CC      tau proteins have improved biological activity, low toxicity, retain the
CC      same or slightly reduced antiviral activity compared with interferon
CC      alpha, and have enhanced antiproliferative activity compared to wild-type
CC      IFN-tau. The method is used for producing IFN-tau proteins with improved
CC      biological activities and properties. These IFN-tau may be administered
CC      to treat cancers and decrease tumour growth, treat viral diseases, treat
CC      autoimmune diseases and treat multiple sclerosis. The cancer or tumour is
CC      selected from the group comprising human adenocarcinoma, breast cancer,
CC      prostate cancer, glioblastomas, melanomas, myelomas, lymphomas,
CC      leukaemia, lung cancer, skin cancer, bladder cancer, kidney cancer, brain
CC      cancer, ovarian cancer, pancreatic cancer, uterine cancer, bone cancer,
CC      colorectal cancer, cervical cancer and neuroectodermal cancer, monoclonal
CC      gammopathies and cervical and oral dysplasia. The autoimmune disease is
CC      selected from Type I diabetes mellitus, rheumatoid arthritis, lupus
CC      erythematosus and/or psoriasis. The viral infection is an RNA virus, a
CC      human immunodeficiency virus (HIV) or hepatitis C virus
XX
XX      Sequence 172 AA:
SQ
Query Match 98.8%; Score 896; DB 4; Length 172;

```

Best Local Similarity 98.8%; Pred. No. 1.8e-91;
Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CYLSRKMLDARENLKLLDRNRLSPHSCLODRKDFGLPQEMVREGDLOQKQAFPPVLYEM 60
DB 1 CYLSRKMLDARENLKLLDRNRLSPHSCLODRKDFGLPQEMVREGDLOQKQAFPPVLYEM 60
QY 61 LQOSFNLFTYEHSSAAMDITLLBOLCTGLQOQDLHDLTCTCRGQGEEDSELGNMDPIVTV 120
DB 61 LQOSFNLFTYEHSSAAMDITLLBOLCTGLQOQDLHDLTCTCRGQGEEDSELGNMDPIVTV 120
QY 121 KKYFGIYDYLQEKGYSDCAMEIVRVMRALTVSTTLQKRLTYMGDLNSP 172
DB 121 KKYFGIYDYLQEKGYSDCAMEIVRVMRALTVSTTLQKRLTYMGDLNSP 172
RESULT 22
AAB31466
ID AAB31466 standard; protein; 172 AA.
XX
AC AAB31466;
DT 20-APR-2001 (first entry)
XX
DE An ovine interferon-tau lmod polypeptide with mutation R5Q.
XX
KM Interferon-tau; IFN-tau; cancer; tumour growth; viral disease;
KM autoimmune disease; multiple sclerosis; adenocarcinoma; breast cancer;
KM prostate cancer; glioblastoma; melanoma; myeloma; lymphoma; leukaemia;
KM lung cancer; skin cancer; bladder cancer; kidney cancer; brain cancer;
KM ovarian cancer; pancreatic cancer; uterine cancer; bone cancer;
KM colorectal cancer; cervical cancer; neuroectodermal cancer; psoriasis;
KM monoclonal gammopathy; dysplasia; diabetes mellitus;
KM rheumatoid arthritis; lupus erythematosus.
XX
KM Synthetic.
OS Ovis sp.
XX
PN WO200078266-A2.
XX
PD 28-DEC-2000.
XX
PF 22-JUN-2000; 2000WO-IB001080.
XX
PR 22-JUN-1999; 99US-0140411P.
XX
PA (UYMA-) UNIV MARYLAND BALTIMORE.
XX
PI Pontzer CH, Shorts LH, Clark CD;
XX
DR WPI; 2001-071357/08.
XX
PT Producing recombinant interferon tau analog proteins with improved
PT properties, useful for treating cancers, autoimmune diseases and viral
PT infections.
XX
PS Claim 15; Page 67-68; 70pp; English.
XX
CC The present sequence represents a mutated ovine interferon-tau lmod
CC polypeptide, which was made using the method of the invention. The
CC specification describes a method of making recombinant interferon (IFN)-
CC tau proteins, which differ from wild-type IFN-tau by amino acid
CC substitutions near the amino terminus of the molecule. The mutated IFN-
CC tau proteins have improved biological activity, low toxicity, retain the
CC same or slightly reduced antiviral activity compared with interferon
CC alpha, and have enhanced antiproliferative activity compared to wild-type
CC IFN-tau. The method is used for producing IFN-tau proteins with improved
CC biological activities and properties. These IFN-tau may be administered
CC to treat cancers and decrease tumour growth, treat viral diseases, treat
CC autoimmune diseases and treat multiple sclerosis. The cancer or tumour is
CC selected from the group comprising human adenocarcinoma, breast cancer,
CC prostate cancer, glioblastomas, melanomas, myelomas, lymphomas,
CC leukaemia, lung cancer, skin cancer, bladder cancer, kidney cancer, brain

CC cancer, ovarian cancer, pancreatic cancer, uterine cancer, bone cancer,
CC colorectal cancer, cervical cancer and neuroectodermal cancer; monoclonal
CC gammopathies and cervical and oral dysplasia. The autoimmune disease is
CC selected from Type I diabetes mellitus, rheumatoid arthritis, lupus
CC erythematosus and/or psoriasis. The viral infection is an RNA virus, a
CC human immuno deficiency virus (HIV) or hepatitis C virus
XX
SQ Sequence 172 AA;
Query Match 98.8%; Score 896; DB 4; Length 172;
Best Local Similarity 98.8%; Pred. No. 1.8e-91;
Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CYLSRKMLDARENLKLLDRNRLSPHSCLODRKDFGLPQEMVREGDLOQKQAFPPVLYEM 60
DB 1 CYLSRKMLDARENLKLLDRNRLSPHSCLODRKDFGLPQEMVREGDLOQKQAFPPVLYEM 60
QY 61 LQOSFNLFTYEHSSAAMDITLLBOLCTGLQOQDLHDLTCTCRGQGEEDSELGNMDPIVTV 120
DB 61 LQOSFNLFTYEHSSAAMDITLLBOLCTGLQOQDLHDLTCTCRGQGEEDSELGNMDPIVTV 120
QY 121 KKYFGIYDYLQEKGYSDCAMEIVRVMRALTVSTTLQKRLTYMGDLNSP 172
DB 121 KKYFGIYDYLQEKGYSDCAMEIVRVMRALTVSTTLQKRLTYMGDLNSP 172
RESULT 23
AAB31464
ID AAB31464 standard; protein; 172 AA.
XX
AC AAB31464;
DT 20-APR-2001 (first entry)
XX
DE An ovine interferon-tau lmod polypeptide with mutation Q31K.
XX
KM Interferon-tau; IFN-tau; cancer; tumour growth; viral disease;
KM autoimmune disease; multiple sclerosis; adenocarcinoma; breast cancer;
KM prostate cancer; glioblastoma; melanoma; myeloma; lymphoma; leukaemia;
KM lung cancer; skin cancer; bladder cancer; kidney cancer; brain cancer;
KM ovarian cancer; pancreatic cancer; uterine cancer; bone cancer;
KM colorectal cancer; cervical cancer; neuroectodermal cancer; psoriasis;
KM monoclonal gammopathy; dysplasia; diabetes mellitus;
KM rheumatoid arthritis; lupus erythematosus.
XX
KM Synthetic.
OS Ovis sp.
XX
PN WO200078266-A2.
XX
PD 28-DEC-2000.
XX
PF 22-JUN-2000; 2000WO-IB001080.
XX
PR 22-JUN-1999; 99US-0140411P.
XX
PA (UYMA-) UNIV MARYLAND BALTIMORE.
XX
PI Pontzer CH, Shorts LH, Clark CD;
XX
DR WPI; 2001-071357/08.
XX
PF N-PSDB; AAF24833.
XX
PT Producing recombinant interferon tau analog proteins with improved
PT properties, useful for treating cancers, autoimmune diseases and viral
PT infections.
XX
PS Claim 15; Page 65-66; 70pp; English.
XX
CC The present sequence represents a mutated ovine interferon-tau lmod
CC polypeptide, which was made using the method of the invention. The
CC specification describes a method of making recombinant interferon (IFN)-
CC tau proteins, which differ from wild-type IFN-tau by amino acid

CC substitutions near the amino terminus of the molecule. The mutated IFN-
CC tau proteins have improved biological activity, low toxicity, retain the
CC same or slightly reduced antiviral activity compared with interferon
CC alpha, and have enhanced antiproliferative activity compared to wild-type
CC IFN-tau. The method is used for producing IFN-tau proteins with improved
CC biological activities and properties. These IFN-tau may be administered
CC to treat cancers and decrease tumour growth, treat viral diseases, treat
CC autoimmune diseases and treat multiple sclerosis. The cancer or tumour is
CC selected from the group comprising human adenocarcinoma, breast cancer,
CC prostate cancer, glioblastomas, melanomas, myelomas, lymphomas,
CC leukaemia, lung cancer, skin cancer, bladder cancer, kidney cancer, brain
CC cancer, ovarian cancer, pancreatic cancer, uterine cancer, bone cancer,
CC colorectal cancer, cervical cancer and neuroendocrine cancer, monoclonal
CC gammaglobulins and cervical and oral dysplasia. The autoimmune disease is
CC selected from Type I diabetes mellitus, rheumatoid arthritis, lupus
CC erythematosus and/or psoriasis. The viral infection is an RNA virus,
CC a human immunodeficiency virus (HIV) or hepatitis C virus
XX
Sequence 172 AA;
90

Query Match	98.8%	Score 896	DB 4	Length 172
Best Local Similarly	98.8%	Pred. No. 1.8e-91		
Matches 170; Conservative	1	Mismatches	0	Gaps 0

Qy 1 CYLSRKLTMDARENLKLTDRMRNLSPHSCLTQDRKDFGLPEQMEWEGDQLQDQAPVLYEM 600
|||||
||| : |||||
Db 1 CYLSRKLTMDARENLKLTDRMRNLSPHSCLTQDRKDFGLPEQMEWEGDQLQDQAPVLYEM 600

Oy	61	LQGSFNLPLYEHSSAAMDITLLLEQLCTGLQOOLDHLDPTCRGVMEEDSELGNMDPIYTV	120
Dd	61	LQGSFNLPLYEHSSAAMDITLLLEQLCTGLQOOLDHLDPTCRGVMEEDSELGNMDPIYTV	120

[illegible]

RESULT 24
AAB31459
ID AAB31459 standard; protein; 172 AA.

AC	AAB31459;
XX	
DT	20-APR-2001 (first entry)

DE An ovine interferon-tau 1mod polypeptide with mutation E13R.

KM Interferon-tau; IFN-tau; cancer; tumour growth; viral disease;
KM autoimmune disease; multiple sclerosis; adenocarcinoma; breast cancer;
KM prostate cancer; glioblastoma; melanoma; myeloma; lymphoma; leukemia;
KM lung cancer; skin cancer; bladder cancer; kidney cancer; brain cancer;
KM ovarian cancer; pancreatic cancer; uterine cancer; bone cancer;
KM colorectal cancer; cervical cancer; neurocutaneous cancer; psoriasis;
KM monoclonal gammopathy; dysplasia; diabetes mellitus;
KM rheumatoid arthritis; lupus erythematosus.

OS Synthetic.
OS Ov1a sp.

PN WO200078266-A2.

PD 28-DEC-2000

PF 22-JUN-2000; 2000WO-1B001080.

PR 22-JUN-1999; 99US-0140411P.

PA (UYMA-) UNIV MARYLAND BALTIMORE.

PI Pontzer CH, Shorts LH, Clark CD;

DR WPI; 2001-071357/08.

DR N-PSDB; AAF24828.

XX Producing recombinant interferon tau analog proteins with improved
PT properties, useful for treating cancers, autoimmune diseases and viral
PT infections.

PS Claim 15; Page 61-62; 70pp; English.

The present sequence represents a mutated ovine interferon-tau 1mod polypeptide, which was made using the method of the invention. The specification describes a method of making recombinant interferon (IFN)-tau proteins, which differ from wild-type IFN-tau by amino acid substitutions near the amino terminus of the molecule. The mutated IFN-tau proteins have improved biological activity, low toxicity, retain the same or slightly reduced antiviral activity compared with interferon alpha, and have enhanced antiproliferative activity compared to wild-type IFN-tau. The method is used for producing IFN-tau proteins with improved biological activities and properties. These IFN-tau may be administered to treat cancers and decrease tumour growth, treat viral diseases, treat autoimmune diseases and treat multiple sclerosis. The cancer or tumour is selected from the group comprising human adenocarcinoma, breast cancer, prostate cancer, glioblastomas, melanomas, myelomas, lymphomas, leukaemia, lung cancer, pancreatic cancer, bladder cancer, kidney cancer, brain cancer, ovarian cancer, skin cancer, uterine cancer, bone cancer, colorectal cancer, cervical cancer and neuroectodermal cancer, monoclonal gammopathies and cervical and oral dysplasia. The autoimmune disease is selected from Type I diabetes mellitus, Rheumatoid arthritis, lupus erythematosus and/or psoriasis. The viral infection is an RNA virus, a human immunodeficiency virus (HIV) or hepatitis C virus.

Sequence 172 AA;

Query Match	98.7%	Score 895;	DB 4;	Length 172;
Best Local Similarity	98.8%	Pred. No. 2.3e-91;		
Matches 170; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy 1 CYLSRKLMDARENLKLLDRNRRLSPHSCLODRKDFGLPQENVEGDOIQKDOAFPVLYEM 60

Db 1 CYLSRKLMDARRNILKLLDRNRRLSPHSCLODRKDFGLPQENVEGDOIQKDOAFPVLYEM 60

[illegible]

Qy	121	KKYFGQIYDYLQEKGYSDCAMEIVR	VEMMALTVSTTLQRLTKMGDLNSP	172
Db	121	KKYFGQIYDYLQEKGYSDCAMEIVR	VEMMALTVSTTLQRLTKMGDLNSP	172

RESULT 25
AAB31467
ID AAB31467 standard; protein; 172 AA

AC AAB31467;

DT 20-APR-2001 (first entry)

DE An ovine interferon-tau 1mod polypeptide with mutation K6T.

KV
interferon- τ ; IFN- τ ; cancer; tumour growth; viral disease;
KX autoimmune disease; multiple sclerosis; adenocarcinoma; breast cancer
KV prostate cancer; glioblastoma; melanoma; kidney cancer; lymphoma; leukemia
KV lung cancer; skin cancer; bladder cancer; thyroid cancer; brain cancer
KV ovarian cancer; pancreatic cancer; uterine cancer; bone cancer;
KV colorectal cancer; cervical cancer; neuroendocrine cancer; psoriasis
KV monoclonal gammopathy; dysplasia; diabetes mellitus;
KV rheumatoid arthritis; lupus erythematosus.

OS Synthetic.

XX

XX

PD 28-DEC-2000.

XX 22-JUN-2000; 2000MO-IB001080.
 XX polypeptide, which was made using the method of the invention. The
 CC specification describes a method of making recombinant interferon (IFN)-
 CC tau proteins, which differ from wild-type IFN-tau by amino acid
 CC substitutions near the amino terminus of the molecule. The mutated IFN-
 CC tau proteins have improved biological activity, low toxicity, retain the
 CC same or slightly reduced antiviral activity compared with interferon
 CC alpha, and have enhanced antiproliferative activity compared to wild-type
 CC IFN-tau. The method is used for producing IFN-tau proteins with improved
 CC biological activities and properties. These IFN-tau may be administered
 CC to treat cancers and decrease tumour growth, treat viral diseases, treat
 CC autoimmune diseases and treat multiple sclerosis. The cancer or tumour is
 CC selected from the group comprising human adenocarcinoma, breast cancer,
 CC prostate cancer, glioblastomas, melanomas, myelomas, lymphomas,
 CC leukaemia, lung cancer, skin cancer, bladder cancer, kidney cancer, brain
 CC cancer, ovarian cancer, pancreatic cancer, uterine cancer, bone cancer,
 CC colorectal cancer, cervical cancer and neuroectodermal cancer, monoclonal
 CC gammaglobulins and cervical and oral dysplasia. The autoimmune disease is
 CC selected from Type I diabetes mellitus, rheumatoid arthritis, lupus
 CC erythematosus and/or psoriasis. The viral infection is an RNA virus, a
 CC human immuno deficiency virus (HIV) or hepatitis C virus
 XX
 SO Sequence 172 AA;
 Query Match 98.6%; Score 894; DB 4; Length 172;
 Best Local Similarity 98.8%; Pred. No. 2.9e-91;
 Matches 170; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CYLSRKMLDARENKILDRMNRSLPHSCLODRKDFGLPQEMVBDQLQKQAPVLYEM 60
 DB 1 CYLSRTMLDARENKILDRMNRSLPHSCLODRKDFGLPQEMVBDQLQKQAPVLYEM 60
 QY 61 LQGSFNLFTYHSSAAMDITLLBQLCTGLQOQDLHDLTCRGQVNGEEDSELGNNDPIYTV 120
 DB 61 LQGSFNLFTYHSSAAMDITLLBQLCTGLQOQDLHDLTCRGQVNGEEDSELGNNDPIYTV 120
 QY 121 KKYFQGIYDYLQEKGYSDCAMEIYRVEMRALTVSTTLQKRLTYKMGDLNSP 172
 DB 121 KKYFQGIYDYLQEKGYSDCAMEIYRVEMRALTVSTTLQKRLTYKMGDLNSP 172
 RESULT 26
 AAB31465 ID AAB31465 standard; protein; 172 AA.
 XX
 XX AAB31465;
 XX 20-APR-2001 (first entry)
 XX
 DE An ovine interferon-tau imod polypeptide with mutation K34H.
 XX
 KW Interferon-tau; IFN-tau; cancer; tumour growth; viral disease;
 KW autoimmune disease; multiple sclerosis; adenocarcinoma; breast cancer;
 KW prostate cancer; glioblastoma; melanoma; myeloma; lymphoma; leukaemia;
 KW lung cancer; skin cancer; bladder cancer; kidney cancer; brain cancer;
 KW ovarian cancer; pancreatic cancer; uterine cancer; bone cancer;

KW colorectal cancer; cervical cancer; neuroectodermal cancer; psoriasis;
 KW monoclonal gammopathy; dysplasia; diabetes mellitus;
 KW rheumatoid arthritis; lupus erythematosus.
 OS Synthetic.
 OS Ovis sp.
 XX WO200078266-A2.
 XX
 XX 28-DEC-2000.
 XX
 XX 22-JUN-2000; 2000MO-IB001080.
 XX polypeptide, which was made using the method of the invention. The
 CC specification describes a method of making recombinant interferon (IFN)-
 CC tau proteins, which differ from wild-type IFN-tau by amino acid
 CC substitutions near the amino terminus of the molecule. The mutated IFN-
 CC tau proteins have improved biological activity, low toxicity, retain the
 CC same or slightly reduced antiviral activity compared with interferon
 CC alpha, and have enhanced antiproliferative activity compared to wild-type
 CC IFN-tau. The method is used for producing IFN-tau proteins with improved
 CC biological activities and properties. These IFN-tau may be administered
 CC to treat cancers and decrease tumour growth, treat viral diseases, treat
 CC autoimmune diseases and treat multiple sclerosis. The cancer or tumour is
 CC selected from the group comprising human adenocarcinoma, breast cancer,
 CC prostate cancer, glioblastomas, melanomas, myelomas, lymphomas,
 CC leukaemia, lung cancer, skin cancer, bladder cancer, kidney cancer, brain
 CC cancer, ovarian cancer, pancreatic cancer, uterine cancer, bone cancer,
 CC colorectal cancer, cervical cancer and neuroectodermal cancer, monoclonal
 CC gammaglobulins and cervical and oral dysplasia. The autoimmune disease is
 CC selected from Type I diabetes mellitus, rheumatoid arthritis, lupus
 CC erythematosus and/or psoriasis. The viral infection is an RNA virus, a
 CC human immuno deficiency virus (HIV) or hepatitis C virus
 XX
 SO Sequence 172 AA;
 Query Match 98.6%; Score 894; DB 4; Length 172;
 Best Local Similarity 98.8%; Pred. No. 2.9e-91;
 Matches 170; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CYLSRKMLDARENKILDRMNRSLPHSCLODRKDFGLPQEMVBDQLQKQAPVLYEM 60
 DB 1 CYLSRKMLDARENKILDRMNRSLPHSCLODRKDFGLPQEMVBDQLQKQAPVLYEM 60
 QY 61 LQGSFNLFTYHSSAAMDITLLBQLCTGLQOQDLHDLTCRGQVNGEEDSELGNNDPIYTV 120
 DB 61 LQGSFNLFTYHSSAAMDITLLBQLCTGLQOQDLHDLTCRGQVNGEEDSELGNNDPIYTV 120
 QY 121 KKYFQGIYDYLQEKGYSDCAMEIYRVEMRALTVSTTLQKRLTYKMGDLNSP 172
 DB 121 KKYFQGIYDYLQEKGYSDCAMEIYRVEMRALTVSTTLQKRLTYKMGDLNSP 172
 RESULT 27
 AAB31460 ID AAB31460 standard; protein; 172 AA.
 XX

AC AAB31460;
 XX
 XX 20-APR-2001 (first entry)
 DT
 DE An ovine interferon-tau 1mod polypeptide with mutation K16M.
 XX
 KM Interferon-tau; IFN-tau; cancer; tumour growth; viral disease;
 KM autoimmune disease; multiple sclerosis; adenocarcinoma; breast cancer;
 KM prostate cancer; glioblastoma; melanoma; lymphoma; leukaemia;
 KM lung cancer; skin cancer; bladder cancer; kidney cancer; brain cancer;
 KM ovarian cancer; pancreatic cancer; uterine cancer; bone cancer;
 KM colorectal cancer; cervical cancer; neuroendocrine cancer; psoriasis;
 KM monoclonal gammopathy; dysplasia; diabetes mellitus;
 KM rheumatoid arthritis; lupus erythematosus.
 KM
 XX Synthetic.
 OS Ovis sp.
 XX
 XX WO200078266-A2.
 XX
 XX 28-DEC-2000.
 XX
 XX 22-JUN-2000; 2000WO-IB001080.
 PF
 XX 22-JUN-1999; 99US-014041P.
 PR
 XX (UYMA-) UNIV MARYLAND BALTIMORE.
 PA
 PI Pontzer CH, Shortz LH, Clark CD;
 XX
 XX WPI: 2001-071357/08.
 DR N-PSDB; AAF24829.
 XX
 PT Producing recombinant interferon tau analog proteins with improved
 PT properties, useful for treating cancers, autoimmune diseases and viral
 PT infections.
 PT
 XX
 XX Claim 15; Page 62-63; 70pp; English.
 PS
 XX The present sequence represents a mutated ovine interferon-tau 1mod
 XX polypeptide, which was made using the method of the invention. The
 XX specification describes a method of making recombinant interferon (IFN)-
 XX tau proteins, which differ from wild-type IFN-tau by amino acid
 XX substitutions near the amino terminus of the molecule. The mutated IFN-
 XX tau proteins have improved biological activity, low toxicity, retain the
 XX same or slightly reduced antiviral activity compared with interferon
 XX alpha, and have enhanced antiproliferative activity compared to wild-type
 XX IFN-tau. The method is used for producing IFN-tau proteins with improved
 XX biological activities and properties. These IFN-tau may be administered
 XX to treat cancers and decrease tumour growth, treat viral diseases, treat
 XX autoimmune diseases and treat multiple sclerosis. The cancer or tumour is
 XX selected from the group comprising human adenocarcinoma, breast cancer,
 XX prostate cancer, glioblastoma, melanoma, myeloma, lymphoma,
 XX leukemia, lung cancer, skin cancer, bladder cancer, kidney cancer, brain
 XX cancer, ovarian cancer, pancreatic cancer, uterine cancer, bone cancer,
 XX colorectal cancer, cervical cancer and neuroendocrine cancer, monoclonal
 XX gammopathies and cervical and oral dysplasia. The autoimmune disease is
 XX selected from Type I diabetes mellitus, rheumatoid arthritis, lupus
 XX erythematosus and/or psoriasis. The viral infection is an RNA virus, a
 XX human immunodeficiency virus (HIV) or hepatitis C virus
 XX
 SQ Sequence 172 AA;
 Query Match 98.6%; Score 894; DB 4; Length 172;
 Best Local Similarity 98.8%; Pred. No. 2.9e-91;
 Matches 170; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 61 LQSFNLFYTHSSAAMDPTLLLEQCTGLQOQLDHLDTCRGQVGEEDSEIGNMDPIYTV 120
 Oy 121 KKYFGIYDYLQEKGYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLSNP 172
 DB 121 KKYFGIYDYLQEKGYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLSNP 172
 RESULT 28
 AAR24944
 ID AAR24944 standard; protein; 195 AA.
 XX
 AC AAR24944;
 XX
 DT 25-MAR-2003 (revised)
 DT 03-JAN-1992 (first entry)
 DE Sequence of ovine trophoblastin variant Xc.
 KM Antiviral; antiinflammatory; antitumour; immunomodulator; immunogen;
 KM trophoblastin; antileukolytic agent.
 XX
 OS Ammoxagus lervia.
 XX
 FH Key location/qualifiers
 FT Peptide 1..23
 FT /label= signal
 XX
 XX WO9209691-A1.
 XX
 XX 11-JUN-1992.
 XX
 XX 29-NOV-1991; 91WO-FR000953.
 PF
 XX 29-NOV-1990; 90FR-00014945.
 PR 29-NOV-1990; 90FR-00014946.
 XX
 PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 XX
 XX Martal J, Degryse E, Gaye P, Charlier M, Charigny G, Reinaud P;
 PI Chaouat G;
 XX
 XX WPI: 1992-217070/26.
 DR
 XX New type I interferon variants with added N-terminal dipeptide - include
 PT expression cassettes providing high yield in yeast, esp. trophoblast
 PT derive, with e.g. anti-leukolytic activity.
 PT
 XX
 PS Claim 7; Page 30; 53pp; French.
 XX
 CC The DNA sequence encoding the precursor of ovine trophoblastin was
 CC disclosed in PCT WO 89/08706 (see AAR24941). AAR24942-R24945 are isoforms
 CC of trophoblastin. They have anti-leukolytic activity and are used to
 CC improve survival of transplanted embryos; as a reagent for detecting
 CC viability of embryos at an early stage of its development; and to improve
 CC the fertility of livestock. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX
 SQ Sequence 195 AA;
 Query Match 98.6%; Score 894; DB 2; Length 195;
 Best Local Similarity 97.7%; Pred. No. 3.5e-91;
 Matches 168; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

RESULT 29
 AAB31461
 ID AAB31461 standard; protein; 172 AA.
 AC AAB31461;
 XX
 DT 20-APR-2001 (first entry)
 DE An ovine interferon-tau lmod polypeptide with mutation D19A.
 XX
 KM Interferon-tau; IFN-tau; cancer; tumour growth; viral disease;
 KM autoimmune disease; multiple sclerosis; adenocarcinoma; breast cancer;
 KM prostate cancer; glioblastoma; melanoma; myeloma; lymphoma; leukaemia;
 KM lung cancer; skin cancer; bladder cancer; kidney cancer; brain cancer;
 KM ovarian cancer; pancreatic cancer; uterine cancer; bone cancer;
 KM colorectal cancer; cervical cancer; neuroectodermal cancer; psoriasis;
 KM monoclonal gammopathy; dysplasia; diabetes mellitus;
 KM rheumatoid arthritis; lupus erythematosus.
 KM
 XX
 OS Synthetic.
 OS Ovis sp.
 PN MO200078266-A2.
 XX
 PD 28-DEC-2000.
 XX
 PF 22-JUN-2000; 2000WO-IB001080.
 XX
 PR 22-JUN-1999; 99US-0140411P.
 XX
 PA (UYMA-) UNIV MARYLAND BALTIMORE.
 P1 Pontzer CH, Shorts LH, Clark CD;
 XX
 DR WPI; 2001-071357/08.
 DR N-PSDB; AAF24830.
 PT Producing recombinant interferon tau analog proteins with improved
 PT properties, useful for treating cancers, autoimmune diseases and viral
 PT infections.
 PS Claim 15; Page 63; 70pp; English.
 XX
 CC The present sequence represents a mutated ovine interferon-tau lmod
 CC polypeptide, which was made using the method of the invention. The
 CC specification describes a method of making recombinant interferon (IFN)-
 CC tau proteins, which differ from wild-type IFN-tau by amino acid
 CC substitutions near the amino terminus of the molecule. The mutated IFN-
 CC tau proteins have improved biological activity, low toxicity, retain the
 CC same or slightly reduced antiviral activity compared with interferon
 CC alpha, and have enhanced antiproliferative activity compared to wild-type
 CC IFN-tau. The method is used for producing IFN-tau proteins with improved
 CC biological activities and properties. These IFN-tau may be administered
 CC to treat cancers and decrease tumour growth, treat viral diseases, treat
 CC autoimmune diseases and treat multiple sclerosis. The cancer or tumour is
 CC selected from the group comprising human adenocarcinoma, breast cancer,
 CC prostate cancer, glioblastomas, melanomas, myelomas, lymphomas,
 CC leukaemia, lung cancer, skin cancer, bladder cancer, kidney cancer, brain
 CC cancer, ovarian cancer, pancreatic cancer, uterine cancer, bone cancer,
 CC colorectal cancer, cervical cancer and neuroectodermal cancer, monoclonal
 CC gammopathies and cervical and oral dysplasia. The autoimmune disease is
 CC selected from Type I diabetes mellitus, rheumatoid arthritis, lupus
 CC erythematosus and/or psoriasis. The viral infection is an RNA virus, a
 CC human immuno deficiency virus (HIV) or hepatitis C virus
 CC
 XX
 SO Sequence 172 AA;
 Query Match 98.3%; Score 892; DB 4; Length 172;
 Best Local Similarity 98.8%; Pred. No. 4.9e-91;
 Matches 170; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CYLSRKIMLDARENTKLLDBMNRSLSPHSCLQDRKDFGLPOEMVGEQDLOXQDAFPVLYEM 60
 Db 1 CYLSRKIMLDARENTKLLARNRSLSPHSCLQDRKDFGLPOEMVGEQDLOXQDAFPVLYEM 60
 QY 61 LOQSFNLFTYHESAAWDTLLBQLCTGLOOQDLHDLDTCRGQVWGEBSDELGNMPTVTY 120
 Db 61 LOQSFNLFTYHESAAWDTLLBQLCTGLOOQDLHDLDTCRGQVWGEBSDELGNMPTVTY 120
 QY 121 KRYFGIYDYLOEGKGYSDCAMEIVRVMRALVTSTLQRLTGMGDLNSP 172
 Db 121 KRYFGIYDYLOEGKGYSDCAMEIVRVMRALVTSTLQRLTGMGDLNSP 172
 RESULT 30
 AAB31463
 ID AAB31463 standard; protein; 172 AA.
 AC AAB31463;
 XX
 DT 20-APR-2001 (first entry)
 DE An ovine interferon-tau lmod polypeptide with mutation P26L.
 XX
 KM Interferon-tau; IFN-tau; cancer; tumour growth; viral disease;
 KM autoimmune disease; multiple sclerosis; adenocarcinoma; breast cancer;
 KM prostate cancer; glioblastoma; melanoma; myeloma; lymphoma; leukaemia;
 KM lung cancer; skin cancer; bladder cancer; kidney cancer; brain cancer;
 KM ovarian cancer; pancreatic cancer; uterine cancer; bone cancer;
 KM colorectal cancer; cervical cancer; neuroectodermal cancer; psoriasis;
 KM monoclonal gammopathy; dysplasia; diabetes mellitus;
 KM rheumatoid arthritis; lupus erythematosus.
 KM
 XX
 OS Synthetic.
 OS Ovis sp.
 PN MO200078266-A2.
 XX
 PD 28-DEC-2000.
 XX
 PF 22-JUN-2000; 2000WO-IB001080.
 XX
 PR 22-JUN-1999; 99US-0140411P.
 XX
 PA (UYMA-) UNIV MARYLAND BALTIMORE.
 P1 Pontzer CH, Shorts LH, Clark CD;
 XX
 DR WPI; 2001-071357/08.
 DR N-PSDB; AAF24832.
 PT Producing recombinant interferon tau analog proteins with improved
 PT properties, useful for treating cancers, autoimmune diseases and viral
 PT infections.
 PS Claim 15; Page 64-65; 70pp; English.
 XX
 CC The present sequence represents a mutated ovine interferon-tau lmod
 CC polypeptide, which was made using the method of the invention. The
 CC specification describes a method of making recombinant interferon (IFN)-
 CC tau proteins, which differ from wild-type IFN-tau by amino acid
 CC substitutions near the amino terminus of the molecule. The mutated IFN-
 CC tau proteins have improved biological activity, low toxicity, retain the
 CC same or slightly reduced antiviral activity compared with interferon
 CC alpha, and have enhanced antiproliferative activity compared to wild-type
 CC IFN-tau. The method is used for producing IFN-tau proteins with improved
 CC biological activities and properties. These IFN-tau may be administered
 CC to treat cancers and decrease tumour growth, treat viral diseases, treat
 CC autoimmune diseases and treat multiple sclerosis. The cancer or tumour is
 CC selected from the group comprising human adenocarcinoma, breast cancer,
 CC prostate cancer, glioblastomas, melanomas, myelomas, lymphomas,
 CC leukaemia, lung cancer, skin cancer, bladder cancer, kidney cancer, brain
 CC cancer, ovarian cancer, pancreatic cancer, uterine cancer, bone cancer,
 CC colorectal cancer, cervical cancer and neuroectodermal cancer, monoclonal

CC gammaglobulins and cervical and oral dysplasia. The autoimmune disease is
 CC selected from Type I diabetes mellitus, rheumatoid arthritis, lupus
 CC erythematous and/or psoriasis. The viral infection is an RNA virus, a
 CC human immunodeficiency virus (HIV) or hepatitis C virus
 XX
 SO Sequence 172 AA:

Query Match 98.1%; Score 890; DB 4; Length 172;
 Best Local Similarity 98.8%; Pred. No. 8.2e-91;
 Matches 170; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CYLSRKMLDARENKLLDRNRLSPHSCLODRKDFGLPQEMVSGDQLQKQAPFVLYEM 60
 Db 1 CYLSRKMLDARENKLLDRNRLSPHSCLODRKDFGLPQEMVSGDQLQKQAPFVLYEM 60
 Oy 61 LQGSFNLFTYHSSAAMDITLLBQLCTGLQOQDLHDLTCRQVNGEEDSELGNMPTVTV 120
 Db 61 LQGSFNLFTYHSSAAMDITLLBQLCTGLQOQDLHDLTCRQVNGEEDSELGNMPTVTV 120
 Oy 121 KKYFGIYDYLQEKGYSDCAMEIVREVMRALTVSTTLQKRLTTKGGDLNSP 172
 Db 121 KKYFGIYDYLQEKGYSDCAMEIVREVMRALTVSTTLQKRLTTKGGDLNSP 172

RESULT 31

AAAP91396 standard; protein; 195 AA.

XX AAP91396;

XX 25-MAR-2003 (revised)
 DT 15-FEB-1990 (first entry)

XX Isoform of Class II alpha-interferon trophoblastine precursor.

XX Antiviral; antitumour.

XX Unidentified.

XX WO8908706-A.

XX 21-SEP-1989.

XX 17-MAR-1989; 89WO-FR000116.

XX 31-JAN-1989; 89US-00304209.

XX (INRG) INRA INST NAT RECH AGRONOMIQUE.

PI Martal J, Charpigny G, Gaye P, Pernollet J, Charlier M;
 PI Guillomot M, Huet JC, Reinaud P;

DR WPI; 1989-292521/40.

PT New isoform(s) of the class II alpha interferon trophoblastine - with
 PT e.g. antiviral, antitumour and immuno-modulating activities, and new DNA
 PT encoding sequences.

PS Claim 11; Page 11; 47pp; French.

XX The isoform (23 kD) can be used for immunological, rejection-inhibiting,
 CC and cell differentiation activities. It can inhibit interleukins at the
 CC start of pregnancy, monitor embryo viability, and protect embryos during
 CC transfer to the womb of a recipient. (Updated on 25-MAR-2003 to correct
 CC PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-
 CC MAR-2003 to correct PI field.)

XX Sequence 195 AA:

Query Match 97.4%; Score 883; DB 1; Length 195;
 Best Local Similarity 97.1%; Pred. No. 5.9e-90;
 Matches 167; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CYLSRKMLDARENKLLDRNRLSPHSCLODRKDFGLPQEMVSGDQLQKQAPFVLYEM 60
 Db 24 CYLSRKMLDARENKLLDRNRLSPHSCLODRKDFGLPQEMVSGDQLQKQAPFVLYEM 83
 Oy 61 LQGSFNLFTYHSSAAMDITLLBQLCTGLQOQDLHDLTCRQVNGEEDSELGNMPTVTV 120
 Db 84 LQGSFNLFTYHSSAAMDITLLBQLCTGLQOQDLHDLTCRQVNGEEDSELGNMPTVTV 143
 Oy 121 KKYFGIYDYLQEKGYSDCAMEIVREVMRALTVSTTLQKRLTTKGGDLNSP 172
 Db 144 KKYFGIYDYLQEKGYSDCAMEIVREVMRALTVSTTLQKRLTTKGGDLNSP 195

RESULT 32

AAAR24943 standard; protein; 195 AA.

XX AR24943;

XX 25-MAR-2003 (revised)
 DT 03-JAN-1992 (first entry)

XX Sequence of ovine trophoblastin variant Xb.

XX Antiviral; antiinflammatory; antitumour; immunomodulator; immunogen;
 KM trophoblastin; antileukolytic agent.

XX Ammotragus lervia.

XX Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= signal

XX WO9209691-A1.

XX 11-JUN-1992.

XX 29-NOV-1991; 91WO-FR000953.

XX 29-NOV-1990; 90FR-00014945.

XX 29-NOV-1990; 90FR-00014946.

XX (INRG) INRA INST NAT RECH AGRONOMIQUE.

PI Martal J, Degryse E, Gaye P, Charlier M, Charpigny G, Reinaud P;
 PI Chaouat G;

DR WPI; 1992-217070/26.

PT New type I interferon variants with added N-terminal dipeptide - include
 PT expression cassettes providing high yield in yeast, esp. trophoblast
 PT derive, with e.g. anti-leukolytic activity.

PS Claim 7; Page 30; 53pp; French.

XX The DNA sequence encoding the precursor of ovine trophoblastin was
 CC disclosed in PCT WO 89/08706 (see AR24941). AR24942-R24945 are isoforms
 CC of trophoblastin. They have anti-leukolytic activity and are used to
 CC improve survival of transplanted embryos; as a reagent for detecting
 CC viability of embryos at an early stage of its development; and to improve
 CC the fertility of livestock. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 195 AA:

Query Match 96.4%; Score 874; DB 2; Length 195;
 Best Local Similarity 96.5%; Pred. No. 6e-89;
 Matches 166; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 1 CYLSRKMLDARENKLLDRNRLSPHSCLODRKDFGLPQEMVSGDQLQKQAPFVLYEM 60
 Db 24 CYLSRKMLDARENKLLDRNRLSPHSCLODRKDFGLPQEMVSGDQLQKQAPFVLYEM 83
 Oy 61 LQGSFNLFTYHSSAAMDITLLBQLCTGLQOQDLHDLTCRQVNGEEDSELGNMPTVTV 120

```

Db      84 LQGSFNLFTYHSSAAMDITLLDQCTGLQQQLDHLDT-CRGQVMGEEDSELGNDPIYTV 143
Oy      121 KKVFQGIYDYLOEKGYSDCAMEIVRVEMMRALTVSTTLQKRLTKMGDLNSP 172
Db      144 KKVFQGIYDYLOEKGYSDCAMEIVRVEMMRALTVSTTLQKRLTKMGDLNSP 195

RESULT 33
AAB49784
ID AAB49784 standard; protein; 196 AA.
XX
AC AAB49784;
XX
DT 23-APR-2001 (first entry)
XX
DE Ovi TP-1 amino acid sequence.
XX
KW Human; keratinocyte derived interferon; KDI; viral infection; lymphoma;
KW immune system related disorder; cancer; multiple sclerosis; AIDS;
KW hepatitis; Cryptosporidium parvum infection; leukaemia; arthritis;
KW diabetes; allergy; chronic myelogenous leukaemia.
XX
OS Synthetic.
XX
PN WO200107608-A1.
XX
PD 01-FEB-2001.
XX
PF 20-JAN-2000; 2000WO-US001239.
XX
PR 21-JUL-1999; 99US-00358587.
PR 21-JUL-1999; 99WO-US016424.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Moore PA, Lafleur DW;
XX
DR WPI; 2001-138557/14.
XX
PT Isolated keratinocyte derived interferon protein and polynucleotide used
PT to prevent, treat or ameliorate an immune system-related disorder, viral
PT infection, viral exposure and cancer.
XX
PS Disclosure; Fig 4; 303pp; English.
XX
XX
CC This invention relates to human polynucleotide sequence AAF72333 which
CC encodes keratinocyte derived interferon (KDI) protein AAB49774, which is
CC a member of the interferon family. AAF72338 represents the codon
CC optimized sequence of KDI. The human KDI gene is located on chromosome 9.
CC The specification includes KDI related protein sequences AAB49775 -
CC AAB49789. Also given in the specification are primer, probe and
CC polynucleotide sequences represented by AAF72334-AAF72370 (excluding
CC AAF72338) which are used in the isolation and characterization of the KDI
CC sequence of the invention. The KDI polypeptide is used to treat viral
CC infections and the protein and polynucleotide may be used to prevent,
CC treat or ameliorate a medical condition such as immune system-related
CC disorder, viral infection, viral exposure and cancer in a mammal.
CC Specific disorders which can be treated by KDI include multiple
CC sclerosis, lymphoma, acquired immune deficiency syndrome, viral
CC hepatitis, Cryptosporidium parvum infection, chronic myelogenous
CC leukaemia, arthritis, diabetes and allergies
XX
SQ Sequence 196 AA;

Query Match      94.5%; Score 857.5; DB 4; Length 196;
Best Local Similarity 94.8%; Pred. No. 4.2e-87;
Matches 164; Conservative 6; Mismatches 2; Indels 1; Gaps 1;
Oy      1 CYLSRKMLDARENIKILDRNRLSPHSCLQDRKDFGLPQEMVSGDQLQKQAPFVLYEM 60
Db      24 CYLSORLMLDARENIKILPEMNRILSPHSCLQDRKDFGLPQEMVSGDQLQKQAPFVLYEM 83

```

```

Oy      61 LQGSFNLFTYHSSAAMDITLLLEQLCTGLQQQLDHLDT-CRGQVMGEEDSELGNDPIYTV 119
Db      84 LQGSFNLFTYHSSAAMDITLLLEQLCTGLQQQLDHLDT-CRGQVMGEEDSELGNDPIYTV 143
Oy      120 VKKFQGIYDYLOEKGYSDCAMEIVRVEMMRALTVSTTLQKRLTKMGDLNSP 172
Db      144 VKKFQGIYDYLOEKGYSDCAMEIVRVEMMRALTVSTTLQKRLTKMGDLNSP 196

RESULT 34
ADF94976
ID ADF94976 standard; protein; 196 AA.
XX
AC ADF94976;
XX
DT 26-FEB-2004 (first entry)
XX
DE Sheep IFN homologue, TP-1, SEQ ID:12.
XX
KW Human keratinocyte derived interferon; human KDI; agonist; antagonist;
KW binding partner identification; immune-related disorder; cancer;
KW viral infection; viral exposure; immunomodulator; virucide; cytostatic;
KW gene therapy; TP-1; ovine; sheep.
XX
OS Ovis aries.
XX
PN WO2003031566-A2.
XX
PD 17-APR-2003.
XX
PF 19-JUL-2002; 2002WO-US023214.
XX
PR 20-JUL-2001; 2001US-00908594.
PR 06-DEC-2001; 2001US-0336165P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Lafleur DW, Moore PA, Ruben SM;
XX
DR WPI; 2003-381702/36.
XX
PT New isolated keratinocyte derived interferon (KDI) polypeptide, useful
PT for preventing, treating or ameliorating a medical condition, such as an
PT immune-related disorder, a viral infection, a viral exposure or cancer.
XX
PS Disclosure; SEQ ID NO 12; 398pp; English.
XX
XX
CC The invention relates to human keratinocyte derived interferon (KDI;
CC ADF94966) and nucleic acids encoding it (ADF94965). The KDI gene is
CC located on chromosome 9q22. The invention also relates to sequences at
CC least 70% identical to the KDI nucleic acid and protein sequences; a
CC polypeptide comprising an epitope-bearing portion of KDI; recombinant
CC vectors and host cells comprising a KDI nucleic acid sequence; a method
CC for the recombinant expression of KDI proteins; a KDI-specific antibody;
CC KDI agonists and antagonists; use of KDI nucleic acids or proteins for
CC treating medical conditions; a method for the diagnosis of a pathological
CC condition or susceptibility to a pathological condition; and methods of
CC screening for KDI binding partners. The KDI polypeptides and
CC polynucleotides, and methods of the invention are useful for preventing,
CC treating or ameliorating a medical condition, such as an immune-related
CC disorder, cancer, or a viral infection or viral exposure. The present
CC sequence is related to the invention.
XX
SQ Sequence 196 AA;

Query Match      94.5%; Score 857.5; DB 7; Length 196;
Best Local Similarity 94.8%; Pred. No. 4.2e-87;
Matches 164; Conservative 6; Mismatches 2; Indels 1; Gaps 1;
Oy      1 CYLSRKMLDARENIKILDRNRLSPHSCLQDRKDFGLPQEMVSGDQLQKQAPFVLYEM 60
Db      24 CYLSORLMLDARENIKILPEMNRILSPHSCLQDRKDFGLPQEMVSGDQLQKQAPFVLYEM 83

```

```

QY 61 LQSFNLFYTHSSAAMDPTTLEQLCTGLQOQLDHLDT-CRGQVMEBDSSELGNDPIVT 119
DB 84 LQOTNLPHTEHSSAAMDPTTLEQLCTGLQOQLDHLDTCCRCQVMEBDSSELGNDPIVT 143
QY 120 VKYFGIYDYLOEKGYSDCAMEIYRVEMMRALTSTTLQKRLTKMGGLNSP 172
DB 144 VKKYFGIYDYLOEKGYSDCAMEIYRVEMMRALTSTTLQKRLTKMGGLNSP 196

RESULT 35
ADSI6363
ID ADSI6363 standard; protein; 152 AA.
XX
AC ADSI6363;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human interferon (IFN) tau (I85L) protein #2.
XX
KM Interferon; IFN; antiviral; antineoplastic; immunomodulator;
KM IFN related disorder; autoimmune disease; multiple sclerosis;
KM diabetes mellitus; lupus erythematosus; Crohn's disease; asthma; allergy;
KM psoriasis; viral infection; hepatitis C; hepatitis B; viral encephalitis;
KM cell proliferation disease; cancer; osteosarcoma; basal cell carcinoma;
KM multiple myeloma; chronic lymphocytic leukaemia; Kaposi's sarcoma;
KM renal-cell carcinoma; ovarian cancer; hairy-cell leukaemia;
KM Hodgkin's disease; gene therapy; human; IFN tau.
XX
OS Homo sapiens.
XX
PN US2004175359-A1.
XX
PD 09-SEP-2004.
XX
PF 30-SEP-2003; 2003US-00677093.
XX
PR 12-NOV-2002; 2002US-0425851P.
XX
PA (DESSU/) DESJARLAIS J R.
PA (MARS/) MARSHALL S A.
PA (MOY/) MO Y.
PA (THOM/) THOMASON A R.
XX
PI Desjarlais JR, Marshall SA, Mo Y, Thomason AR;
XX
DR WPI; 2004-642104/62.
XX
PT Novel type 1 interferon (IFN) having antiviral, antineoplastic or
PT immunomodulatory activity same as wild-type IFN, and being circularly
PT permuted or cyclized to provide modulated characteristics, useful for
PT treating IFN related diseases.
XX
PS Disclosure; SEQ ID NO 54; 48bp; English.
XX
CC The present invention relates to a type 1 interferon (IFN) comprising
CC antiviral, antineoplastic and immunomodulatory activity similar to a
CC naturally occurring IFN and has been circularly permuted or cyclised and
CC has at least one modulated characteristic as compared to the naturally
CC occurring IFN. The invention is useful for treating IFN related disorder
CC which includes autoimmune diseases such as multiple sclerosis, diabetes
CC mellitus, lupus erythematosus, Crohn's disease, asthma, allergies and
CC psoriasis, viral infections such as hepatitis C, hepatitis B and viral
CC osteosarcoma, basal cell carcinoma, multiple myeloma, chronic lymphocytic
CC leukaemia, Kaposi's sarcoma, renal-cell carcinoma, ovarian cancer, hairy-
CC cell leukaemia and Hodgkin's disease. The invention is also useful in
CC gene therapy. The present sequence is human interferon (IFN) protein.
XX
SQ Sequence 152 AA;

```

```

QY 1 CYLSRKLMDARENIKLLDRNRLSPHSCLDRKDFGLPQEMVSGDQLQKQAPFVLYEM 60
DB 1 CYLSRKLMDARENIKLLDRNRLSPHSCLDRKDFGLPQEMVSGDQLQKQAPFVLYEM 60
QY 61 LQSFNLFYTHSSAAMDPTTLEQLCTGLQOQLDHLDT-CRGQVMEBDSSELGNDPIVT 120
DB 61 LQSFNLFYTHSSAAMDPTTLEQLCTGLQOQLDHLDT-CRGQVMEBDSSELGNDPIVT 108
QY 121 KKYFGIYDYLOEKGYSDCAMEIYRVEMMRALTSTTLQKRLTK 164
DB 109 KKYFGIYDYLOEKGYSDCAMEIYRVEMMRALTSTTLQKRLTK 152

RESULT 36
AAB49783
ID AAB49783 standard; protein; 195 AA.
XX
AC AAB49783;
XX
DT 23-APR-2001 (first entry)
XX
DE Bovine TP-1 amino acid sequence.
XX
KM Human; keratinocyte derived interferon; KDI; viral infection; lymphoma;
KM immune system related disorder; cancer; multiple sclerosis; AIDS;
KM hepatitis; Cryptosporidium parvum infection; leukaemia; arthritis;
KM diabetes; allergy; chronic myelogenous leukaemia.
XX
OS Bos sp.
XX
PN WO200107608-A1.
XX
PD 01-FEB-2001.
XX
PF 20-JAN-2000; 2000WO-US001239.
XX
PR 21-JUL-1999; 99US-00358587.
PR 21-JUL-1999; 99WO-US016424.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Moore PA, Lafleur DW;
XX
DR WPI; 2001-138557/14.
XX
PT Isolated keratinocyte derived interferon protein and polynucleotide used
PT to prevent, treat or ameliorate an immune system-related disorder, viral
PT infection, viral exposure and cancer.
XX
PS Disclosure; Fig 4; 303pp; English.
XX
CC This invention relates to human polynucleotide sequence AAF72333 which
CC encodes keratinocyte derived interferon (KDI) protein AAB49774, which is
CC a member of the interferon family. AAF72338 represents the codon
CC optimised sequence of KDI. The human KDI gene is located on chromosome 9.
CC The specification includes KDI related protein sequences AAB49775 -
CC AAB49789. Also given in the specification are primer, probe and
CC polynucleotide sequences represented by AAF72334-AAF72370 (excluding
CC AAF72338) which are used in the isolation and characterisation of the KDI
CC sequence of the invention. The KDI polypeptide is used to treat viral
CC infections and the protein and polynucleotide may be used to prevent,
CC treat or ameliorate a medical condition such as immune system-related
CC disorder, viral infection, viral exposure and cancer in a mammal.
CC Specific disorders which can be treated by KDI include multiple
CC sclerosis, lymphoma, acquired immune deficiency syndrome, viral
CC hepatitis, Cryptosporidium parvum infection, chronic myelogenous
CC leukaemia, arthritis, diabetes and allergies
XX
SQ Sequence 195 AA;

```

Query Match 86.7%; Score 786; DB 8; Length 152;
 Best Local Similarity 92.7%; Pred. No. 2,9e-79;
 Matches 152; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

Query Match 79.7%; Score 723; DB 4; Length 195;
 Best Local Similarity 80.7%; Pred. No. 4.4e-72;

Matches	138:	Conservative	14:	Mismatches	19:	Indels	0:	Gaps	0:
QY	1	CYLSRKTLMDARENIKLLDRNRRLSPHSCLODRKDFGLPOEWEVGDOLOKDOAFVLYEM	60						
Db	24	CYLSRDLMLGARENRLRLARNRRLSPHPCLODRKDFGLPOEWEVGNOLOKDOALISVLIHEM	83						
QY	61	LOQSFNLFYETHSNAAWDTTLLEQLCTGLQOQLDHLDTCRGVMEEDSELGNDPIYTV	120						
Db	84	LOQCENLFYETHSNAAWMTTLLEQLCTGLQOQLDHLDTCLGVMEGKSDMGKMGPIILTV	143						
QY	121	KKYFGQIYDYOEKGYSDCAWEIYVENMRALTVSTTLQKRLTKGGDINS	171						
Db	144	KKYFGIHVLYLKEKEYSDCAWEIIMEMMRALSSSTTLQKRLRKGGDINS	194						
RESULT 37									
ID	ABB08641	standard; protein; 195 AA.							
XX	ABB08641;								
AC	25-APR-2002	(first entry)							
DT									
XX									
DE		Bovine interferon tau SEQ ID NO 10.							
XX									
KW		Bovine; interferon; tau; IFN; antiviral; antitumour.							
XX									
OS		Bos taurus.							
PN		JP2001342199-A.							
XX									
PD		11-DEC-2001.							
XX									
PF		29-MAR-2001; 2001JP-00096242.							
XX									
PR		30-MAR-2000; 2000JP-00093383.							
XX									
XX		(NORQ) NORINSUISANSO KACHIKU EISEI.							
PA		(DAUC) DAICHI PHARM CO LTD.							
PA		(KATA) KATAKURA IND CO LTD.							
XX									
DR		WPI; 2002-145115/19.							
XX									
XX		N-PSDB; ABA97931.							
PT									
PT		Preparation of purified interferon, for use in antiviral and antitumor							
XX		agents, from recombinant baculovirus containing the interferon gene.							
PS		Disclosure; Page 11-12; 13pp; Japanese.							
XX									
CC		The invention relates to preparation of purified interferon (IFN) in							
CC		which a raw material containing IFN, prepared by infecting a recombinant							
CC		baculovirus with a gene encoding IFN protein, is subjected to a treatment							
CC		including silica gel chromatography, anion exchange column chromatography							
CC		and metal chelate column chromatography. IFN is used as an active							
CC		component in antiviral agents and antitumor agents. The present sequence							
CC		is that of bovine interferon-tau							
XX									
XX									
SQ		Sequence 195 AA;							
QY	Query Match	79.7%; Score 723; DB 5; Length 195;							
	Best Local Similarity	80.7%; Pred. No. 4,4e-72;							
	Matches 138; Conservative	14; Mismatches 19; Indels	0; Gaps	0;					
Db	1	CYLSRKTLMDARENIKLLDRNRRLSPHSCLODRKDFGLPOEWEVGDOLOKDOAFVLYEM	60						
	24	CYLSRDLMLGARENRLRLARNRRLSPHPCLODRKDFGLPOEWEVGNOLOKDOALISVLIHEM	83						
QY	61	LOQSFNLFYETHSNAAWDTTLLEQLCTGLQOQLDHLDTCRGVMEEDSELGNDPIYTV	120						
Db	84	LOQCENLFYETHSNAAWMTTLLEQLCTGLQOQLDHLDTCLGVMEGKSDMGKMGPIILTV	143						
QY	121	KKYFGQIYDYOEKGYSDCAWEIYVENMRALTVSTTLQKRLTKGGDINS	171						
Db	144	KKYFGIHVLYLKEKEYSDCAWEIIMEMMRALSSSTTLQKRLRKGGDINS	194						
QY	121	KKYFGQIYDYOEKGYSDCAWEIYVENMRALTVSTTLQKRLTKGGDINS	171						

```

Db      144 KKVGQGIHVYIKKEXEYSDCAMEIIRMEMMRALSSSTTLQKRLRKKGDLNS 194

RESULT 38
ADFP94975
ID      ADFP94975 standard; protein, 195 AA.
XX
AC      ADFP94975;
XX
DT      26-FEB-2004 (first entry)
DE      Bovine IFN homologue, TP-1, SEQ ID:11.
XX
KW      Human keratinocyte derived interferon; human KDI; agonist; antagonist;
KW      inducing pattern identification; immune-related disorder; cancer;
KW      viral infection; viral exposure; immunomodulator; virocid; cytostatic;
KW      gene therapy; TP-1; bovine; cow.
XX
OS      Bos taurus.
XX
PN      WO2003031566-A2.
XX
PD      17-APR-2003.
XX
PF      19-JUL-2002; 2002WO-US023214.
PR      20-JUN-2001; 2001US-00908594.
PR      06-DEC-2001; 2001US-0336165P.
XX
PA      (HUMA-) HUMAN GENOME SCI INC.
XX
PI      Lafleur DW, Moore PA, Ruben SM;
DR      WPI; 2003-381702/36.
XX
PT      New isolated keratinocyte derived interferon (KDI) polypeptide, useful
PT      for preventing, treating or ameliorating a medical condition, such as an
PT      immune-related disorder, a viral infection, a viral exposure or cancer.
XX
PS      Disclosure; SEQ ID NO 11; 398pp; English.
XX
CC      The invention relates to human keratinocyte derived interferon (KDI;
CC      ADFP94966) and nucleic acids encoding it (ADFP94965). The KDI gene is
CC      located on chromosome 9q22. The invention also relates to sequences at
CC      least 70% identical to the KDI nucleic acid and protein sequences; a
CC      polypeptide comprising an epitope-bearing portion of KDI; recombinant
CC      vectors and host cells comprising a KDI nucleic acid sequence; a method
CC      for the recombinant expression of KDI proteins; a KDI-specific antibody;
CC      KDI agonists and antagonists; use of KDI nucleic acids or proteins for
CC      treating medical conditions; a method for the diagnosis of a pathological
CC      condition or susceptibility to a pathological condition; and methods of
CC      screening for KDI binding partners. The KDI polypeptides and
CC      polynucleotides, and methods of the invention are useful for preventing,
CC      treating or ameliorating a medical condition, such as an immune-related
CC      disorder, cancer, or a viral infection or viral exposure. The present
CC      sequence is related to the invention.
XX
SQ      Sequence 195 AA:

Query Match          79.7%; Score 723; DB 7; Length 195;
Best Local Similarity 80.7%; Pred. No. 4,4e-72;
Matches 138; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

    1 CYLSRKMLDIRENUKLILDRNRRLSPSCLDORXDFGLPOEWVEGDLOLQKDAPFVLYEM 60
    24 CYLESDHMLGKREURILRRNRRLSPHCLODRKDFGLPOEWBESNLQAKDAISVLHEM 83
    61 LQGSFNLFYTESSHSAAMDITLLLEQLCTGLAQOOLPHLDTCRGVNGEEDSELGNMDPIVTV 120
    84 LQQCFNFLFYTESSHSAAMNTTILEQLCTGLAQOOLELDLDCGLGPVNGEKSDMGKMGPIITLV 143
    121 KKIFRGIVDYIOEGKGYSDCAMEIYRVEMRALITYSTTLQKRLTKGGDLNS 171

```

DB 144 KRYFGIHYVLEKEKYSDCAMEIIRMEMRALSSTTLQKRLKRGDLS 194

RESULT 39
AA04539
ID AAR04539 standard; protein; 195 AA.
XX
AC AAR04539;
XX
DT 25-MAR-2003 (revised)
DT 17-SEP-1990 (first entry)
XX
DE cDNA clone of sequence encoding bovine trophoblast protein-1 (bTP-1).
XX
KM Bovine trophoblast protein-1; bTP-1; fertility; da.
XX
OS Sus acrofa.
XX
PN EP367063-A.
XX
PD 09-MAY-1990.
XX
PF 23-OCT-1989; 89EP-00119642.
XX
PR 26-OCT-1988; 88US-00262870.
XX
PA (UMOR) UNIV MISSOURI.
XX
PI Roberts MR, Imakawa K;
XX
DR WPI; 1990-141062/19.
DR N-PSDB; AA004285.
XX
PT Recombinant bovine trophoblast protein-1 - used for enhancing fertility
XX or treating viral diseases in mammal, esp. cattle.
XX
PS Claim 3; Fig 1; 27pp; English.
XX
CC The bTP-1 produced from the gene may be used to promote fertility or
CC treat viral disease in cattle. The gene may also be used to provide
CC transgenic animals with enhanced fertility, or in prophylactic and
CC therapeutic treatment of other mammals. (Updated on 25-MAR-2003 to
CC correct PA field.)
XX
SQ Sequence 195 AA;

Query Match 79.4%; Score 720; DB 2; Length 195;
Best Local Similarity 80.7%; Pred. No. 9.5e-72;
Matches 138; Conservative 13; Mismatches 20; Indels 0; Gaps 0;

OY 1 CYLSRKLMDARENLKLDNRNRLSPHSCLODRKDFGLPQEMVEGDLQKQDAFPVLYEM 60
DB 24 CYLSEDHNLGARENLRLARNRRLSPHPCLODRKDFGLPQEMVEGDLQKQDAISVLHEM 83
OY 61 LQGSFNLFYTEHSSAANDTTLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNDPIVTV 120
DB 84 LQOCLNFYTEHSSAANDTTLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNDPIVTV 143
OY 121 KRYFGIHYVLEKEKYSDCAMEIIRMEMRALSSTTLQKRLKRGDLS 171
DB 144 KRYFGIHYVLEKEKYSDCAMEIIRMEMRALSSTTLQKRLKRGDLS 194

RESULT 40
AA070809
ID AAM70809 standard; protein; 173 AA.
XX
AC AAM70809;
XX
DT 04-FEB-1999 (first entry)
XX
DE A tau modified interferon protein oh-IFN-tau-d3.
XX

KM Tau modified interferon protein; oh-IFN-tau-d3; antiviral activity;
KM Interferon activity; antitumor; autoimmune disease.
XX
XX Unidentified.
XX
PN JP10295382-A.
XX
PD 10-NOV-1998.
XX
PF 24-APR-1997; 97JP-00106941.
XX
PR 24-APR-1997; 97JP-00106941.
XX
PA (SANY) SANKYO CO LTD.
XX
DR WPI; 1999-038279/04.
DR N-PSDB; AAV70626.
XX
PT An interferon tau modified body - used as e.g. an antiviral agent.
XX
PS Claim 2; Page 14; 29pp; Japanese.
XX
CC The present sequence represents a tau modified interferon protein
CC designated oh-IFN-tau-d3. The interferon tau modified protein has a high
CC antiviral activity and is low in cytotoxicity. The protein has interferon
CC activity, and can be used as an antiviral agent, an antitumor agent, or
CC creating an autoimmune disease
XX
SQ Sequence 173 AA;

Query Match 76.2%; Score 691; DB 2; Length 173;
Best Local Similarity 76.2%; Pred. No. 1.4e-68;
Matches 131; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

OY 1 CYLSRKLMDARENLKLDNRNRLSPHSCLODRKDFGLPQEMVEGDLQKQDAFPVLYEM 60
DB 2 CYLSRKLMDARENLKLDNRNRLSPHSCLODRKDFGLPQEMVEGDLQKQDAISVLHEM 61
OY 61 LQGSFNLFYTEHSSAANDTTLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNDPIVTV 120
DB 62 LQGSFNLFYTEHSSAANDTTLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNDPIVTV 121
OY 121 KRYFGIHYVLEKEKYSDCAMEIIRMEMRALSSTTLQKRLKRGDLS 172
DB 122 KRYFGIHYVLEKEKYSDCAMEIIRMEMRALSSTTLQKRLKRGDLS 173

RESULT 41
ADG42697
ID ADG42697 standard; protein; 171 AA.
XX
AC ADG42697;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human interferon tau-1 precursor.
XX
KM Human; NOVX; GAGE-like protein; interferon; GPCR; mast cell protease;
KM hepatocyte nuclear factor; cancer; immune disorder; hepatic disorder;
KM truma; HIV; Parkinson's disease; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN US2003202971-A1.
XX
PD 30-OCT-2003.
XX
PF 06-MAY-2002; 2002US-00139854.
XX
PR 15-FEB-2000; 2000US-0182723P.
PR 15-FEB-2000; 2000US-0182724P.
PR 15-FEB-2000; 2000US-0182733P.
PR 22-FEB-2000; 2000US-0183986P.

CC Manufacture of medicaments to treat proliferative disorders (e.g. cancer
CC and mastocytosis), immune disorders, hepatic disorders (e.g. cirrhosis),
CC viral infections (e.g. AIDS and hepatitis), disorders of the neuro-
CC olfactory system (e.g. trauma, surgery and/or neoplastic disorders),
CC adenocarcinoma, lymphoma, asthma, Crohn's disease, multiple sclerosis and
CC also for treating Abiright hereditary osteodysplasia. Accordingly, they
CC exhibit cytotoxic, immunosuppressive, hepatotropic, virucide, anti-HIV,
CC antiinflammatory, vulnerary, antidiabetic and neuroprotective
CC activities. This peptide is homologous to a fragment of a human NOVX
CC protein of the invention.

XX SQ Sequence 171 AA;

Query Match 71.6%; Score 649; DB 7; Length 171;
Best Local Similarity 80.9%; Pred. No. 6.7e-64;
Matches 123; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 CYLSRKLMDARENLKLDNRNRLSPHSCLODRKDFGLPQWVEGDQLQKQAPVLYEM 60
DB 20 CYLSEDMGLGARENRLRLARNRRLSPHSCLODRKDFGLPQWVEGNGQLQKQALSVLHEM 79

QY 61 LQGSFNLFTYTHSSAAMDITLLEQLCTGLQOQLDHLDTCRQVNGEBSDELGNDDPIVTV 120
DB 80 LQGSFNLFTYTHSSAAMDITLLEQLCTGLQOQLDHLDTCRQVNGEBSDELGNDDPIVTV 139

QY 121 KKYFQGIYDIQOEKGYSDCAMEIVREMMRL 152
DB 140 KKYFQGIHVIKKEKYSDCAMEIIRVEMRL 171

RESULT 43
ADM76604
ID ADM76604 standard; protein, 171 AA.
XX
AC ADM76604;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human NOVX protein-related protein fragment SegID58.
XX
XX NOVX; cytotoxic; immunosuppressive; virucide; anti-HIV; hepatotropic;
KM antiinflammatory; neuroprotective; hepatotropic; antiparkinsonian;
KM gene therapy; vaccine; NOVX-associated disorder; cancer; immune disorder;
KM viral infection; AIDS; hepatitis; neurological disorder;
KM Alzheimer's disease; Parkinson's disease; olfactory disorder;
KM chromosome mapping; tissue typing; NOVX; human.
XX
OS Homo sapiens.
XX
PN WO2004009634-A2.
XX
PD 29-JAN-2004.
XX
PF 04-OCT-2001; 2001WO-US031284.
XX
XX 04-OCT-2000; 2000US-02378662P.
PR 02-JAN-2001; 2001US-0259414P.
PR 18-JAN-2001; 2001US-0262454P.
PR 14-FEB-2001; 2001US-00783429.
PR 03-JUL-2001; 2001US-00898953.
PR 03-OCT-2001; 2001US-00970607.
XX
XX (CURA-) CURAGEN CORP.
XX
PI Gerlach VL, Ellerman K, MacDougall JR, Smithson G, Shinkets RA,
PI Raetelli L, Herrmann J;
XX
XX WPI; 2004-143267/14.
XX
XX New NOVX polypeptides and nucleic acid molecules useful for diagnosing,
PT preventing or treating NOVX-associated disorders (e.g. cancer, AIDS or
PT Alzheimer's disease), and in chromosome mapping, tissue typing or
PT pharmacogenetics.

XX PS Disclosure; SEQ ID NO 58; 173pp; English.
XX
XX This invention relates to novel NOVX polypeptides and the DNA sequences
XX which encode them. The invention may be useful for the development of
XX compounds with a cytotoxic, immunosuppressive, virucide, anti-HIV,
XX hepatotropic, antiinflammatory, neuroprotective, nootropic or
XX antiparkinsonian activity. In addition, the disclosed sequences may be
XX useful for gene therapy or development of a vaccine. The NOVX
XX polypeptide, nucleic acid or antibody is useful in the manufacture of a
XX medicament for treating a syndrome associated with a human disease. These
XX are used in diagnosing, treating or preventing NOVX-associated disorders
XX such as cancer, immune disorders, viral infections (for example AIDS or
XX hepatitis), neurological disorders (for example Alzheimer's disease or
XX Parkinson's disease) or olfactory disorders. The nucleic acids are
XX further used as hybridisation probes, in chromosome mapping, tissue
XX typing, preventive medicine, and pharmacogenetics. The present sequence
XX is that of a human protein fragment which was used to demonstrate
XX homology between the NOVX proteins of the invention and other human
XX proteins.

XX SQ Sequence 171 AA;

Query Match 71.6%; Score 649; DB 8; Length 171;
Best Local Similarity 80.9%; Pred. No. 6.7e-64;
Matches 123; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 CYLSRKLMDARENLKLDNRNRLSPHSCLODRKDFGLPQWVEGDQLQKQAPVLYEM 60
DB 20 CYLSEDMGLGARENRLRLARNRRLSPHSCLODRKDFGLPQWVEGNGQLQKQALSVLHEM 79

QY 61 LQGSFNLFTYTHSSAAMDITLLEQLCTGLQOQLDHLDTCRQVNGEBSDELGNDDPIVTV 120
DB 80 LQGSFNLFTYTHSSAAMDITLLEQLCTGLQOQLDHLDTCRQVNGEBSDELGNDDPIVTV 139

QY 121 KKYFQGIYDIQOEKGYSDCAMEIVREMMRL 152
DB 140 KKYFQGIHVIKKEKYSDCAMEIIRVEMRL 171

RESULT 44
AAW70808
ID AAW70808 standard; protein, 173 AA.
XX
AC AAW70808;
XX
DT 04-FEB-1999 (first entry)
XX
XX A tau modified interferon protein oh-IFN-tau-d2.
XX
XX Tau modified interferon protein; oh-IFN-tau-d2; antiviral activity;
KM interferon activity; antitumor; autoimmune disease.
XX
XX Unidentified.
XX
XX JP10295382-A.
XX
PN 10-NOV-1998.
XX
PD 24-APR-1997; 97JP-00106941.
XX
PF 24-APR-1997; 97JP-00106941.
XX
PR 24-APR-1997; 97JP-00106941.
XX
XX (SANY) SANKYO CO LTD.
XX
PI WPI; 1999-038279/04.
XX
DR N-PSDB; AAW70625.
XX
XX An interferon tau modified body - used as e.g. an antiviral agent.
PT Claim 1; Page 13; 29pp; Japanese.
XX
XX The present sequence represents a tau modified interferon protein

RESULT 47	
AAW56433	
ID	AAW56433 standard; protein; 173 AA.
XX	
AC	AAW56433;
XX	
DT	03-AUG-1998 (first entry)
XX	
DE	Amino acid sequence of an interferon-tau variant protein.
XX	
KW	Human; interferon-tau; hIFN-tau; variant; treatment; prevention;
KW	viral infection; tumour; autoimmune disease.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	Protein
FT	Misc-difference 28
FT	Misc-difference 59
FT	Misc-difference 59
FT	/note= "His encoded by CAC"
FT	/note= "His encoded by CAC"
XX	
PN	W09807863-A1.
XX	
PD	26-FEB-1998.
XX	
PF	20-AUG-1997; 97WO-JP002879.
XX	
PR	21-AUG-1996; 96JP-00219879.
XX	
PA	(SANY) SANKYO CO LTD.
XX	
PI	Ishimura M, Nishigaki T;
XX	
DR	WPI, 1998-169167/15.
DR	N-PSDB; AAV22980.
XX	
PT	Polypeptides with interferon activity - for treatment and prevention of
PT	viral infection, tumours and autoimmune diseases.
XX	
PS	Claim 4; Page 30-31; 61pp; Japanese.
XX	
CC	The present sequence represents a human interferon-tau (hIFN-tau)
CC	variant. The hIFN-tau variant protein is used for the treatment and
CC	prevention of viral infections, tumours and autoimmune diseases
XX	
SO	Sequence 173 AA;
SO	
Query Match	69.2%; Score 628; DB 2; Length 173;
Best Local Similarity	69.8%; Pred. No. 1.5e-61;
Matches 120; Conservative	21; Mismatches 31; Indels 0; Gaps 0
QY	1 CYLSRKLMDARENIKLDIRNRRSLPHSCLODRKDFGLPQEKVEGDLOKQDAFVLYEM 60
DB	2 CDLSQHHVLVSRKNRLLDEMRRSLPHFCLQDRKDFALPQEKVEGGOLOEQAISVLHEM 61
QY	61 LOOSFNLEPYTHSSAAMPDTTLLEOLCTGLQOOLDLHLCRCGVMGEEDSESGNMDPIYTV 120
DB	62 LOOSFNLEPYTHSSAAMPDTTLLEOLCTGLHQQLDNLDAICLGVMGEEDSALGRTPTTAL 121
QY	121 KKYFGIYDYLQEKGYSDCAEIVEVMNRALVTSTLQKRLTRKGGDINSP 172
DB	122 KRYFGIHVYLKEKGYSDCAEIVTALIMRSPSSLISQERLRMMGDGLSSP 173
RESULT 48	
AAW70812	
ID	AAW70812 standard; protein; 173 AA.
XX	
AC	AAW70812;
XX	

[illegible]

XX WO9807863-A1.
 PN
 XX
 PD 26-FEB-1998.
 XX
 PF 20-AUG-1997; 97WO-JP002879.
 XX
 PR 21-AUG-1996; 96JP-00219879.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 PI Ishimura M, Nishigaki T;
 XX
 DR WPI; 1998-169167/15.
 XX
 DR N-PSDB; AAV22981.
 XX
 PT Polypeptides with interferon activity - for treatment and prevention of
 PT viral infection, tumours and autoimmune diseases.
 XX
 PS Claim 5; Page 33-34; 61pp; Japanese.
 XX
 CC The present sequence represents a human interferon-tau (hIFN-tau)
 CC variant. The hIFN-tau variant protein is used for the treatment and
 CC prevention of viral infections, tumours and autoimmune diseases
 XX
 SEQ Sequence 173 AA;

Query Match	69.1%	Score 627	DB 2	Length 173
Best Local Similarity	69.8%	Pred. No. 2e-61		
Matches 120; Conservative	21	Mismatches	0	Gaps 0

[illegible]

RESULT 50	
AAW70813	
ID	AAW70813 standard; protein; 173 AA.

AC AAW70813;

DT 04-FEB-1999 (first entry)

DE A human interferon-tau-d2 (hIFN-tau-d2) protein.

KM Tau modified interferon protein; IFN-tau-d2; antiviral activity;
KM interferon activity; antitumor; autoimmune disease.

OS Homo sapiens.

PN JP10295382-A.

PD 10-NOV-1998.

PF 24-APR-1997; 97JP-00106941.

PR 24-APR-1997; 97JP-00106941.

PA (SANY) SANKYO CO LTD.

DR WPI; 1999-038279/04.

XX

PT An interferon tau modified body - used as e.g. an antiviral agent.

XX Disclosure; Page 24-25; 29pp; Japanese.
 PS
 CC The present sequence represents human interferon-tau-d2 (hIFN-tau-d2).
 CC The protein is used in the course of the invention to create interferon
 CC tau modified proteins which have a high antiviral activity and are low in
 CC cytotoxicity. The protein has interferon activity, and can be used as an
 CC antiviral agent, an antitumor agent, or treating an autoimmune disease
 XX
 XX Sequence 173 AA;
 SQ

Query Match	Score	DB 2	Length
69.1%	627	173	

Matches 120; Conservative 21; Mismatches 31; Indels 0; Gaps 0;

```

QY      1 CYLSKMLDLDRBNKLLDRMKRSLSPHSGLQORXQFGLPQEWVEGQLOKQOAFPLVLEM 60
      2 CDLSQHYHLVGRKNRLDDEMRRLSPHFLQDRKQFALPQEWVEGQLOEQAQISVLHEM 61
Db
QY      61 LQGSNNLFTYTHSSAAMPDTLLLEQLCTGLQOQDLHDLPTRGQVMGESEBELGMDDIVY 120
      62 LQGSNNLFTYTHSSAAMPDTLLLDQCTGLHQOQDLNDNDALGQVMGESEBALGRTGPTLAL 121
Db
QY      121 KKYFGIYDYLQEKGYSDCAWEIIVAVEMMRALVTSTLQKRLTKWGGDINSP 172
      122 KRYFGIHYVLYKEKGYSDCAWEIYVLEIMRFSYLSISQERLRIMDGDJLSP 173
Db

```

Search completed: October 5, 2005, 10:34:35
Job time : 181 secs

Job time : 181 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 5, 2005, 10:23:15 ; Search time 41 Seconds

(without alignments)
403.641 Million cell updates/sec

Title: US-10-694-247-2

Perfect score: 907
Sequence: 1 CYLSRKLMDARENLKULDR.....TVSTTLQKRLTKMGDLSNP 172

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

PIR 79:*
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	897	98.9	195	2 JS0204	ctrophoblast interf
2	880	97.0	195	2 I47068	ctrophoblast protei
3	868	95.7	195	2 I47066	ctrophoblast protei
4	865	95.4	195	2 I47069	ctrophoblast protei
5	847	93.4	172	2 A61578	ctrophoblast protei
6	846	93.3	195	2 I46272	ctrophoblast interf
7	842	92.8	195	2 A61455	ctrophoblast protei
8	806	88.9	195	2 I47067	ctrophoblast protei
9	778	85.8	195	2 I47097	ctrophoblast protei
10	745	82.1	184	2 I47098	ctrophoblast protei
11	724	79.8	195	2 A39505	ctrophoblast interf
12	723	79.7	195	2 S23751	ctrophoblast interf
13	720	79.4	195	2 A40068	ctrophoblast protei
14	720	79.4	195	2 B39505	ctrophoblast protei
15	609	67.1	195	2 A53746	interferon, tropho
16	608	67.0	195	2 A61403	interferon alpha-I
17	587	64.7	195	2 I47070	interferon omega -
18	585	64.5	195	2 I46397	interferon alpha -
19	582	64.2	195	1 IVBO11	interferon alpha-I
20	513.5	56.6	190	2 S23711	interferon alpha-I
21	499	55.0	195	1 IVHO22	interferon alpha-I
22	497	54.8	110	2 B61578	ctrophoblast protei
23	488.5	53.9	190	2 S23712	interferon alpha-I
24	473	52.1	195	1 IVHUI1	interferon omega-I
25	469.5	51.8	179	2 S23710	interferon alpha-I
26	454	50.1	189	2 I51970	interferon precurs
27	446	49.2	176	2 I56314	interferon alpha -
28	444	49.0	195	1 IVHO21	interferon alpha-I
29	440	48.5	189	1 IVHUI4	interferon alpha-I

30	440	48.5	189	1 IVHUI7	interferon alpha-5
31	438	48.3	189	1 IVHUI9	interferon alpha-1
32	431	47.5	167	2 D25843	interferon alpha-G
33	431	47.5	195	2 I46398	interferon alpha -
34	429	47.3	189	1 IVHUI4B	interferon alpha-I
35	429	47.3	189	1 IVHUI5	interferon alpha-5
36	428	47.2	189	1 IVHUI1	interferon alpha-1
37	427	47.1	195	2 I46975	interferon-omega20
38	426	47.0	195	2 I46972	interferon-omega44
39	425	46.9	189	2 I52347	interferon alpha-M
40	424	46.7	195	2 I46974	interferon-omega45
41	423	46.6	195	2 S70011	interferon type I
42	421	46.4	181	2 I56313	interferon alpha 2
43	421	46.4	189	2 I84454	interferon-alpha-F
44	419	46.2	167	2 E25843	interferon alpha-F
45	419	46.2	189	1 IVHUIF	interferon alpha-I
46	408	45.0	184	1 IVHOA2	interferon alpha-I
47	405	44.7	189	2 F25843	interferon alpha-J
48	405	44.7	189	1 IVHUI0	interferon alpha-7
49	404	44.5	189	2 I53102	interferon-alpha-J
50	403	44.4	184	1 IVHOA1	interferon alpha-I
51	403	44.4	184	1 IVHOA3	interferon alpha-I
52	403	44.4	184	1 IVHOA4	interferon alpha-I
53	398	43.9	189	1 IVHUI6	interferon alpha-I
54	397.5	43.8	165	2 I78570	alpha 2 interferon
55	394.5	43.5	188	1 IVHUI2	interferon alpha-2
56	392	43.2	189	2 I37584	IFN-alpha-N-protei
57	386	42.6	189	1 IVHUI8	interferon alpha-I
58	384	42.3	189	1 IVMSA5	interferon alpha-I
59	384	42.3	189	2 S23709	interferon alpha-1
60	380	41.9	190	2 A24401	interferon alpha-I
61	378	41.7	189	1 IVHUI6	interferon alpha-I
62	378	41.7	190	2 I49775	interferon alpha-B
63	377	41.6	162	2 C25843	interferon alpha-4
64	377	41.6	189	1 IVHUI4	interferon alpha-4
65	376	41.5	189	1 IVBO11	interferon alpha-I
66	375	41.3	189	1 IVMSA1	interferon alpha-I
67	374	41.2	190	2 I49772	interferon alpha-7
68	372	41.0	190	1 IVMSA2	interferon alpha-2
69	371	40.9	192	1 IVRTA1	interferon alpha-I
70	368	40.6	189	1 IVBO1D	interferon alpha-I
71	364	40.1	190	2 JH0468	interferon alpha-1
72	364	40.1	190	2 I49774	alpha-interferon -
73	360	39.7	189	1 IVBO1B	interferon alpha-I
74	355	39.1	189	1 IVBO1A	interferon alpha-I
75	351	38.7	189	1 IVBO1C	interferon alpha-I
76	342	37.7	189	1 IVMSA6	interferon alpha-I
77	340.5	37.5	194	2 JS0664	interferon precurs
78	340	37.5	189	2 I49773	murine interferon
79	331.5	36.5	186	1 IVMSA4	interferon alpha-I
80	318	35.1	187	2 I46206	interferon-alpha -
81	316	34.8	187	2 I46204	interferon-alpha -
82	287.5	31.7	186	1 IVBO22	interferon beta-2
83	257	28.3	186	1 IVBOB1	interferon beta-I
84	255	28.1	186	1 IVBOB3	interferon beta-3
85	253.5	27.9	187	1 IVHUI1	interferon beta-1
86	250.5	27.6	170	2 A48772	interferon, atypic
87	230.5	25.4	186	1 IVBOB1	interferon beta-1
88	180.5	19.9	90	2 I57395	interferon alpha-2
89	174	19.0	72	2 I79343	interferon alpha T
90	172.5	19.0	184	2 JC5424	interferon beta pr
91	164	18.1	182	1 IVMSB	interferon beta pr
92	141	15.5	66	2 I58939	interferon alpha N
93	134.5	14.8	193	2 I50693	interferon - chick
94	133.5	14.7	191	2 S57642	interferon precurs
95	110.5	12.2	72	2 I73333	interferon alpha-2
96	110	12.1	58	2 I79344	interferon alpha O
97	107.5	11.9	72	2 I73332	interferon alpha-2
98	85	9.4	1920	2 A53188	pericentrin - mous
99	83	9.2	741	2 T48006	hypothetical prote
100	81.5	9.0	239	2 G96740	hypothetical prote
101	80.5	8.9	581	2 S63183	CNN1 protein - yea
102	80.5	8.9	1269	2 F84730	probable myosin he

103	80	8.8	2042	2	T18339	variant-specific s
104	79.5	8.8	344	2	B80401	cofactor biosynthe
105	79.5	8.8	379	2	H82284	queuine tRNA-ribos
106	79.5	8.8	3026	2	T28431	variant surface pr
107	78	8.6	489	2	S05474	keratin 8, type II
108	78	8.6	3255	2	G81702	adherence factor T
109	77.5	8.5	1029	2	T41386	RanBP7/importin-be
110	77	8.5	576	1	B35128	DNA repair and gen
111	76.5	8.4	115	2	B71029	hypothetical prote
112	76.5	8.4	614	2	T29902	hypothetical prote
113	76.5	8.4	1131	2	AD2166	two-component sens
114	76	8.4	519	2	A89903	conserved hypotnet
115	75	8.3	634	2	C81652	Arp-dependent heli
116	75	8.3	561	2	G71818	probable thiophene
117	75	8.3	4502	2	A33547	keratin, type II c
118	74.5	8.2	374	2	AG0387	queuine tRNA-ribos
119	74.5	8.2	545	2	H83079	hypothetical prote
120	74	8.2	481	2	H87282	conserved hypotnet
121	74	8.2	1802	2	T00020	bacterial blight-r
122	73.5	8.1	269	2	F89455	protein F55A4.4 [i
123	73.5	8.1	478	2	T02034	RNA-directed RNA p
124	73.5	8.1	1006	2	T26770	hypothetical prote
125	73	8.0	534	2	F96713	unknown protein T6
126	73	8.0	1073	2	S14032	kinesin-related pr
127	73	8.0	1085	2	T38378	kinesin-like prote
128	73	8.0	1938	2	JC5421	smooth muscle myos
129	72	8.0	1972	2	JC5420	smooth muscle myos
130	72.5	8.0	822	2	S56801	hypothetical prote
131	72.5	8.0	980	2	T00045	cellodextrin phosp
132	72.5	8.0	1642	2	T08880	MDMA receptor-bind
133	72.5	8.0	2168	2	T30171	keratin 8, type II
134	72	7.9	487	2	JT0407	ninein - mouse
135	72	7.9	490	2	J50558	cytokeratin EndoA
136	72	7.9	674	2	C81505	hypothetical prote
137	72	7.9	680	2	E72033	hypothetical prote
138	72	7.9	680	2	B86590	hypothetical prote
139	72	7.9	756	2	T05829	hypothetical prote
140	72	7.9	758	2	T32861	hypothetical prote
141	72	7.9	781	2	T05206	hypothetical prote
142	72	7.9	796	2	C85220	hypothetical prote
143	72	7.9	4589	2	T14914	dynein beta heavy
144	72	7.9	4924	2	T50176	probable peptide s
145	71.5	7.9	353	2	T05552	SREI protein-relat
146	71.5	7.9	522	2	D96764	unknown protein F2
147	71.5	7.9	559	2	B72487	hypothetical prote
148	71.5	7.9	607	2	S77082	hypothetical prote
149	71.5	7.9	658	2	T50080	probable DNA repair
150	71.5	7.9	829	2	T46556	exonuclease ABC c
151	71.5	7.9	829	2	G96900	DNA topoisomerase
152	71.5	7.9	830	2	G96900	DNA gyrase (topois
153	71.5	7.9	856	2	T58411	protein-tyrosine k
154	71.5	7.9	863	2	C88546	protein R107.4 [im
155	71.5	7.9	894	1	A41527	protein-tyrosine k
156	71.5	7.9	2023	2	T13154	polycomb protein e
157	71.5	7.9	2136	2	B84651	hypothetical prote
158	71	7.8	226	2	C90711	probable response
159	71	7.8	226	2	B64796	transcription regu
160	71	7.8	226	2	C85561	Shigella regulator
161	71	7.8	310	2	S43865	cytokeratin 8, typ
162	71	7.8	372	2	T51082	hypothetical prote
163	71	7.8	505	1	S76229	DNA repair protein
164	71	7.8	722	2	AD2222	Arp-dependent heli
165	71	7.8	757	2	D95103	X-pro dipeptidyl-p
166	71	7.8	780	2	T77941	hypothetical prote
167	71	7.8	795	2	B97971	x-pro dipeptidyl-p
168	71	7.8	806	2	G71805	leucine-cRNA ligas
169	71	7.8	2819	2	A90551	conserved hypotnet
170	70.5	7.8	248	2	T23708	hypothetical prote
171	70.5	7.8	415	2	H84718	hypothetical prote
172	70.5	7.8	558	2	E72220	conserved hypotnet
173	70.5	7.8	656	2	S73313	hypothetical prote
174	70.5	7.8	660	2	C84099	exonuclease ABC (
175	70.5	7.8	839	2	C97250	preprotein translo
176	70.5	7.8	863	2	S37040	paramyosin - tapew
177	70.5	7.8	892	2	A56213	DNA excision-repai
178	70.5	7.8	1039	2	F71427	hypothetical prote
179	70.5	7.8	1046	2	T29776	hypothetical prote
180	70	7.7	179	2	B83903	RNA polymerase ECF
181	70	7.7	332	2	AD2384	transposase alr462
182	70	7.7	399	2	B75201	hypothetical prote
183	70	7.7	448	2	A36311	70K u small nucle
184	70	7.7	584	2	A97171	uncharacterized pr
185	70	7.7	600	4	A56379	Zp3 receptor precu
186	70	7.7	609	2	T22803	hypothetical prote
187	70	7.7	725	1	JC5016	hyaluronan recepto
188	70	7.7	1067	2	H75139	isoleucyl-tRNA syn
189	70	7.7	2677	2	A38194	desmoplakin I - hu
190	69.5	7.7	452	2	S77436	sigma factor sigma
191	69.5	7.7	610	2	A10466	ATP-dependent DNA
192	69.5	7.7	822	2	A80238	haemin storage sys
193	69.5	7.7	822	2	T47007	hypothetical prote
194	69.5	7.7	866	2	F64625	type I restriction
195	69.5	7.7	942	2	S23251	protein-tyrosine k
196	69.5	7.7	1139	2	T23018	hypothetical prote
197	69.5	7.7	1707	2	AH2085	two-component hybr
198	69	7.6	272	2	S16325	homeotic protein A
199	69	7.6	346	2	D90156	conserved hypotnet
200	69	7.6	425	2	E64403	translational releas
201	69	7.6	483	2	A34720	keratin 8, type II
202	69	7.6	513	2	C82366	conserved hypotnet
203	69	7.6	670	2	A83255	exonuclease ABC s
204	69	7.6	715	2	S77439	hypothetical prote
205	69	7.6	996	1	S42208	NAD ADP-riboyltra
206	69	7.6	1153	2	B97718	hypothetical prote
207	69	7.6	1237	2	A31334	phosphorylase kina
208	69	7.6	1972	1	A41604	myosin heavy chain
209	68.5	7.6	153	2	B82153	hypothetical prote
210	68.5	7.6	209	2	B72247	ribosomal protein
211	68.5	7.6	367	1	A46355	site-specific DNA-
212	68.5	7.6	392	1	RN25P	polymease-aassocia
213	68.5	7.6	431	2	A48094	serum and glucocor
214	68.5	7.6	442	2	S73472	probable thiophene
215	68.5	7.6	487	2	G71432	hypothetical prote
216	68.5	7.6	504	2	S48550	hypothetical prote
217	68.5	7.6	590	2	A10174	probable lon prote
218	68.5	7.6	694	2	A53978	protein-tyrosine-p
219	68.5	7.6	795	2	S30874	hypothetical prote
220	68.5	7.6	836	2	S49940	cell division cont
221	68.5	7.6	875	2	B71850	type I restriction
222	68.5	7.6	935	2	T50774	probable translati
223	68.5	7.6	948	2	C82077	glutamate-ammonia
224	68.5	7.6	1039	2	C64418	isoleucine-cRNA 11
225	68.5	7.6	1132	2	T44001	major DNA binding
226	68.5	7.6	1162	2	T30194	nuclear protein SA
227	68.5	7.6	2291	1	A46147	spectrin beta chain
228	68	7.5	244	2	H75107	hypothetical prote
229	68	7.5	316	2	A41781	proteoglycan-Lb -
230	68	7.5	325	2	S18575	svrm protein - Rhi
231	68	7.5	326	2	A45505	svrm protein - Rhi
232	68	7.5	326	2	F95319	svrm transcription
233	68	7.5	338	2	A13183	aldo/keto reductas
234	68	7.5	349	2	T38904	ATPA-binding prote
235	68	7.5	380	2	D64129	secretin receptor
236	68	7.5	440	2	JC2532	secretin receptor
237	68	7.5	489	2	A47200	EcoA system protei
238	68	7.5	493	2	F86133	hypothetical prote
239	68	7.5	493	2	C91282	hypothetical prote
240	68	7.5	583	2	C84788	probable myosin he
241	68	7.5	809	2	F81312	leucine-cRNA ligas
242	68	7.5	839	1	TVHUV	transforming prote
243	68	7.5	842	2	S56819	hypothetical prote
244	68	7.5	848	1	S64732	scaffold attachmen
245	68	7.5	908	2	T50685	seca protein limpo
246	68	7.5	994	2	T49276	c-mec tyrosine kin
247	68	7.5	1063	2	T18255	cytoskeleton assem
248	68	7.5	2139	2	T18296	myosin heavy chain

249	68	7.5	5255	2	T31677	322	66	7.3	1181	2	C82500	ImcF-related prote
250	67.5	7.4	109	2	F75105	323	66	7.3	1289	2	I84505	calcium-dependent
251	67.5	7.4	135	2	T29473	324	66	7.3	1610	2	T11681	hypothetical prote
252	67.5	7.4	300	2	E96585	325	66	7.3	1953	2	S63244	BN11 protein - yea
253	67.5	7.4	394	2	T19181	326	66	7.3	2524	2	A35844	XorC protein - Af
254	67.5	7.4	457	2	T05651	327	65	7.2	206	2	A64095	ribosomal protein
255	67.5	7.4	773	2	T00554	328	65.5	7.2	252	2	F89869	conserved hypothet
256	67.5	7.4	846	2	A86663	329	65.5	7.2	300	2	S50727	sporulation protei
257	67.5	7.4	916	2	D81072	330	65.5	7.2	351	2	A10991	cell division prot
258	67.5	7.4	1092	2	T12520	331	65.5	7.2	364	2	D90699	probable capule a
259	67.5	7.4	1138	2	T24635	332	65.5	7.2	364	2	G85549	probable capule a
260	67.5	7.4	1964	2	A59282	333	65.5	7.2	364	2	F64781	Ybb8 protein - Bac
261	67.5	7.4	2147	2	T21328	334	65.5	7.2	375	2	D97268	toxic anion resist
262	67	7.4	234	1	J00506	335	65.5	7.2	375	2	A50552	queuine tRNA-ribos
263	67	7.4	244	2	A40625	336	65.5	7.2	378	2	A82083	phosphonate metabo
264	67	7.4	268	2	T24253	337	65.5	7.2	387	2	T36697	hypothetical prote
265	67	7.4	293	2	F70329	338	65.5	7.2	405	2	T47595	RING finger protei
266	67	7.4	326	2	T51811	339	65.5	7.2	430	2	B40646	folyl-polyglutamat
267	67	7.4	391	2	H90308	340	65.5	7.2	463	2	T16503	hypothetical prote
268	67	7.4	437	2	S52014	341	65.5	7.2	465	2	T27415	hypothetical prote
269	67	7.4	484	2	C88264	342	65.5	7.2	496	2	AC1306	carboxy-terminal p
270	67	7.4	488	2	I44330	343	65.5	7.2	566	2	F70028	transmembrane rece
271	67	7.4	501	2	G84314	344	65.5	7.2	803	2	H87197	penicillin binding
272	67	7.4	503	2	I46015	345	65.5	7.2	846	2	JN0324	lysine aminopeptid
273	67	7.4	535	2	S74703	346	65.5	7.2	846	2	S23157	membrane alanyl am
274	67	7.4	629	2	A28666	347	65.5	7.2	913	2	S61580	probable membrane
275	67	7.4	629	2	F86351	348	65.5	7.2	932	2	G68857	isoleucyl-tRNA t11
276	67	7.4	798	2	S62031	349	65.5	7.2	944	2	A10507	isoleucyl-tRNA t11
277	67	7.4	891	2	B84614	350	65.5	7.2	1013	2	T31211	tyrc protein homol
278	67	7.4	931	2	B75027	351	65.5	7.2	1015	2	AF2061	hypothetical prote
279	67	7.4	941	2	B53335	352	65.5	7.2	1088	2	T18559	hypothetical prote
280	67	7.4	1008	2	A82304	353	65.5	7.2	1127	2	T22404	hypothetical prote
281	67	7.4	1066	2	F71100	354	65.5	7.2	1164	2	T03814	tumor suppressor p
282	67	7.4	1241	2	S40528	355	65.5	7.2	1866	1	GWME2C	genome polyprotein
283	67	7.4	1278	2	B70236	356	65.5	7.2	2101	2	A42184	nuclear mitotic ap
284	67	7.4	1805	1	A64224	357	65	7.2	220	2	E75090	adenylate kinase (
285	66.5	7.3	382	2	A64057	358	65	7.2	337	2	F83715	indirect positive
286	66.5	7.3	439	2	AD2555	359	65	7.2	358	2	S44261	SRI1 protein - Ara
287	66.5	7.3	494	2	T46442	360	65	7.2	370	2	A25004	keratin, 53k type
288	66.5	7.3	513	1	ZABP4	361	65	7.2	393	2	E30272	transposase tSC11
289	66.5	7.3	534	2	F95202	362	65	7.2	405	2	C33697	transposase (01) B
290	66.5	7.3	537	2	F98069	363	65	7.2	405	2	A33781	transposase (01) B
291	66.5	7.3	562	2	S61295	364	65	7.2	405	2	D83826	transposase (01) B
292	66.5	7.3	563	2	T30087	365	65	7.2	405	2	B83845	transposase (01) B
293	66.5	7.3	597	2	B53978	366	65	7.2	405	2	A83891	transposase (01) B
294	66.5	7.3	600	2	B81401	367	65	7.2	405	2	B83893	transposase (01) B
295	66.5	7.3	608	2	T02299	368	65	7.2	405	2	A84042	transposase (01) B
296	66.5	7.3	760	2	A40195	369	65	7.2	408	2	G83745	transposase (01) B
297	66.5	7.3	876	2	I49152	370	65	7.2	410	2	AD2087	gas vesicle protei
298	66.5	7.3	880	1	JC4166	371	65	7.2	437	2	S74591	Sensory transducti
299	66.5	7.3	880	2	B53743	372	65	7.2	441	2	F63680	transposase (01) B
300	66.5	7.3	916	2	G81797	373	65	7.2	441	2	F63683	transposase (01) B
301	66.5	7.3	1110	2	T49091	374	65	7.2	441	2	B83796	transposase (01) B
302	66.5	7.3	1195	2	E96615	375	65	7.2	441	2	C83813	transposase (01) B
303	66	7.3	158	2	A12064	376	65	7.2	441	2	T44292	transposase (01) B
304	66	7.3	214	2	B64378	377	65	7.2	451	1	S75229	hypothetical prote
305	66	7.3	234	2	T52100	378	65	7.2	459	2	F83996	transposase (01) B
306	66	7.3	237	2	A83759	379	65	7.2	463	2	H84118	transposase (01) B
307	66	7.3	258	2	S75726	380	65	7.2	469	2	A99577	conserved hypothet
308	66	7.3	287	2	T26411	381	65	7.2	536	2	B84549	probable ubiquitin
309	66	7.3	340	2	T49006	382	65	7.2	552	2	D82878	phosphomannomutase
310	66	7.3	375	2	E85536	383	65	7.2	597	2	D87665	methyl-accepting C
311	66	7.3	375	2	C38530	384	65	7.2	621	2	S10450	myosin heavy chain
312	66	7.3	375	2	A99686	385	65	7.2	636	2	A45949	mezzozote surface
313	66	7.3	390	2	A60093	386	65	7.2	654	2	T21618	hypothetical prote
314	66	7.3	399	2	T23470	387	65	7.2	668	2	S64123	hypothetical prote
315	66	7.3	553	2	G83866	388	65	7.2	715	2	S73637	ATP-dependent prot
316	66	7.3	562	2	G70002	389	65	7.2	738	2	S35093	plakoglobin - Afri
317	66	7.3	786	2	I49274	390	65	7.2	763	2	F95125	ATP-dependent DNA
318	66	7.3	846	2	E81328	391	65	7.2	763	2	C97996	ATP-dependent DNA
319	66	7.3	853	1	S20595	392	65	7.2	799	2	T00331	hypothetical prote
320	66	7.3	1031	1	A38713	393	65	7.2	881	2	AD2580	two component sens
321	66	7.3	1054	2	B38919	394	65	7.2	881	2	C97362	protein sensor pro

395	65	7.2	894	1	FAHUA2	alpha-actinin 2 -
396	65	7.2	930	2	A95193	isolectin-1bRn
397	65	7.2	930	2	E98059	isolectin-1bRn
398	65	7.2	941	2	S78633	isolectin-1bRn
399	65	7.2	991	2	H86168	hypothetical prote
400	65	7.2	992	2	S32902	6-phosphofructokin
401	65	7.2	1076	2	S44764	C27D1.1 protein -
402	65	7.2	1277	2	E70224	hypothetical prote
403	65	7.2	1276	2	A39401	metalloproteinase
404	65	7.2	1276	2	A39401	metalloproteinase
405	65	7.2	1276	2	A39401	metalloproteinase
406	65	7.2	1276	2	A39401	metalloproteinase
407	65	7.2	1276	2	A39401	metalloproteinase
408	65	7.2	1276	2	A39401	metalloproteinase
409	65	7.2	1276	2	A39401	metalloproteinase
410	65	7.2	1276	2	A39401	metalloproteinase
411	65	7.2	1276	2	A39401	metalloproteinase
412	65	7.2	1276	2	A39401	metalloproteinase
413	65	7.2	1276	2	A39401	metalloproteinase
414	65	7.2	1276	2	A39401	metalloproteinase
415	65	7.2	1276	2	A39401	metalloproteinase
416	65	7.2	1276	2	A39401	metalloproteinase
417	65	7.2	1276	2	A39401	metalloproteinase
418	65	7.2	1276	2	A39401	metalloproteinase
419	65	7.2	1276	2	A39401	metalloproteinase
420	65	7.2	1276	2	A39401	metalloproteinase
421	65	7.2	1276	2	A39401	metalloproteinase
422	65	7.2	1276	2	A39401	metalloproteinase
423	65	7.2	1276	2	A39401	metalloproteinase
424	65	7.2	1276	2	A39401	metalloproteinase
425	65	7.2	1276	2	A39401	metalloproteinase
426	65	7.2	1276	2	A39401	metalloproteinase
427	65	7.2	1276	2	A39401	metalloproteinase
428	65	7.2	1276	2	A39401	metalloproteinase
429	65	7.2	1276	2	A39401	metalloproteinase
430	65	7.2	1276	2	A39401	metalloproteinase
431	65	7.2	1276	2	A39401	metalloproteinase
432	65	7.2	1276	2	A39401	metalloproteinase
433	65	7.2	1276	2	A39401	metalloproteinase
434	65	7.2	1276	2	A39401	metalloproteinase
435	65	7.2	1276	2	A39401	metalloproteinase
436	65	7.2	1276	2	A39401	metalloproteinase
437	65	7.2	1276	2	A39401	metalloproteinase
438	65	7.2	1276	2	A39401	metalloproteinase
439	65	7.2	1276	2	A39401	metalloproteinase
440	65	7.2	1276	2	A39401	metalloproteinase
441	65	7.2	1276	2	A39401	metalloproteinase
442	65	7.2	1276	2	A39401	metalloproteinase
443	65	7.2	1276	2	A39401	metalloproteinase
444	65	7.2	1276	2	A39401	metalloproteinase
445	65	7.2	1276	2	A39401	metalloproteinase
446	65	7.2	1276	2	A39401	metalloproteinase
447	65	7.2	1276	2	A39401	metalloproteinase
448	65	7.2	1276	2	A39401	metalloproteinase
449	65	7.2	1276	2	A39401	metalloproteinase
450	65	7.2	1276	2	A39401	metalloproteinase
451	65	7.2	1276	2	A39401	metalloproteinase
452	65	7.2	1276	2	A39401	metalloproteinase
453	65	7.2	1276	2	A39401	metalloproteinase
454	65	7.2	1276	2	A39401	metalloproteinase
455	65	7.2	1276	2	A39401	metalloproteinase
456	65	7.2	1276	2	A39401	metalloproteinase
457	65	7.2	1276	2	A39401	metalloproteinase
458	65	7.2	1276	2	A39401	metalloproteinase
459	65	7.2	1276	2	A39401	metalloproteinase
460	65	7.2	1276	2	A39401	metalloproteinase
461	65	7.2	1276	2	A39401	metalloproteinase
462	65	7.2	1276	2	A39401	metalloproteinase
463	65	7.2	1276	2	A39401	metalloproteinase
464	65	7.2	1276	2	A39401	metalloproteinase
465	65	7.2	1276	2	A39401	metalloproteinase
466	65	7.2	1276	2	A39401	metalloproteinase
467	65	7.2	1276	2	A39401	metalloproteinase
468	64	7.1	918	2	C96829	unknown protein F1
469	64	7.1	959	2	S61155	hypothetical prote
470	64	7.1	1179	2	E98012	hypothetical prote
471	64	7.1	1611	2	A84743	probable myosin he
472	64	7.1	1909	2	A45592	liver stage antigen
473	64	7.1	2244	2	F90563	hypothetical prote
474	64	7.1	3006	2	T28625	variant-specific s
475	64	7.1	3225	2	I52300	giantin - human
476	64	7.1	3259	1	A56539	giantin - human
477	64	7.1	3259	1	A56539	giantin - human
478	64	7.1	3259	1	A56539	giantin - human
479	64	7.1	3259	1	A56539	giantin - human
480	64	7.1	3259	1	A56539	giantin - human
481	64	7.1	3259	1	A56539	giantin - human
482	64	7.1	3259	1	A56539	giantin - human
483	64	7.1	3259	1	A56539	giantin - human
484	64	7.1	3259	1	A56539	giantin - human
485	64	7.1	3259	1	A56539	giantin - human
486	64	7.1	3259	1	A56539	giantin - human
487	64	7.1	3259	1	A56539	giantin - human
488	64	7.1	3259	1	A56539	giantin - human
489	64	7.1	3259	1	A56539	giantin - human
490	64	7.1	3259	1	A56539	giantin - human
491	64	7.1	3259	1	A56539	giantin - human
492	64	7.1	3259	1	A56539	giantin - human
493	64	7.1	3259	1	A56539	giantin - human
494	64	7.1	3259	1	A56539	giantin - human
495	64	7.1	3259	1	A56539	giantin - human
496	64	7.1	3259	1	A56539	giantin - human
497	64	7.1	3259	1	A56539	giantin - human
498	64	7.1	3259	1	A56539	giantin - human
499	64	7.1	3259	1	A56539	giantin - human
500	64	7.1	3259	1	A56539	giantin - human
501	64	7.1	3259	1	A56539	giantin - human
502	64	7.1	3259	1	A56539	giantin - human
503	64	7.1	3259	1	A56539	giantin - human
504	64	7.1	3259	1	A56539	giantin - human
505	64	7.1	3259	1	A56539	giantin - human
506	64	7.1	3259	1	A56539	giantin - human
507	64	7.1	3259	1	A56539	giantin - human
508	64	7.1	3259	1	A56539	giantin - human
509	64	7.1	3259	1	A56539	giantin - human
510	64	7.1	3259	1	A56539	giantin - human
511	64	7.1	3259	1	A56539	giantin - human
512	64	7.1	3259	1	A56539	giantin - human
513	64	7.1	3259	1	A56539	giantin - human
514	64	7.1	3259	1	A56539	giantin - human
515	64	7.1	3259	1	A56539	giantin - human
516	64	7.1	3259	1	A56539	giantin - human
517	64	7.1	3259	1	A56539	giantin - human
518	64	7.1	3259	1	A56539	giantin - human
519	64	7.1	3259	1	A56539	giantin - human
520	64	7.1	3259	1	A56539	giantin - human
521	64	7.1	3259	1	A56539	giantin - human
522	64	7.1	3259	1	A56539	giantin - human
523	64	7.1	3259	1	A56539	giantin - human
524	64	7.1	3259	1	A56539	giantin - human
525	64	7.1	3259	1	A56539	giantin - human
526	64	7.1	3259	1	A56539	giantin - human
527	64	7.1	3259	1	A56539	giantin - human
528	64	7.1	3259	1	A56539	giantin - human
529	64	7.1	3259	1	A56539	giantin - human
530	64	7.1	3259	1	A56539	giantin - human
531	64	7.1	3259	1	A56539	giantin - human
532	64	7.1	3259	1	A56539	giantin - human
533	64	7.1	3259	1	A56539	giantin - human
534	64	7.1	3259	1	A56539	giantin - human
535	64	7.1	3259	1	A56539	giantin - human
536	64	7.1	3259	1	A56539	giantin - human
537	64	7.1	3259	1	A56539	giantin - human
538	64	7.1	3259	1	A56539	giantin - human
539	64	7.1	3259	1	A56539	giantin - human
540	64	7.1	3259	1	A56539	giantin - human

541	63	6.9	767	1	CORPCD	614	62	6.8	118	2	B69382	hypothetical prote
542	63	6.9	799	2	T02656	615	62	6.8	179	2	B83727	hypothetical prote
543	63	6.9	829	2	T01362	616	62	6.8	201	2	A41656	clindamycin resist
544	63	6.9	832	2	T38749	617	62	6.8	213	2	G64203	chymidine kinase (
545	63	6.9	923	2	T08033	618	62	6.8	213	2	F82968	hypothetical prote
546	63	6.9	925	2	T29311	619	62	6.8	240	2	T09700	MADS-box protein -
547	63	6.9	979	2	T40006	620	62	6.8	246	2	B71084	hypothetical prote
548	63	6.9	987	1	T08830	621	62	6.8	268	2	C90516	esterase/lipase 1
549	63	6.9	1028	2	A96719	622	62	6.8	293	2	AC1459	conserved hypotet
550	63	6.9	1076	2	A69409	623	62	6.8	314	2	G97050	DNA-methyltransfer
551	63	6.9	1093	1	S50614	624	62	6.8	326	2	S42531	hem B protein - Sy
552	63	6.9	1095	2	T41171	625	62	6.8	344	2	B95123	conserved hypotet
553	63	6.9	1095	2	AC9059	626	62	6.8	344	2	G97993	hypothetical prote
554	63	6.9	1225	2	A49464	627	62	6.8	358	2	S73776	MG269 homolog F11
555	63	6.9	1284	2	G86145	628	62	6.8	365	2	T08679	procollagen-lysin
556	63	6.9	1405	2	T40607	629	62	6.8	384	1	T46966	diene cytochrome
557	63	6.9	1478	2	T38712	630	62	6.8	390	2	A72108	hypothetical prote
558	63	6.9	1620	2	S21045	631	62	6.8	390	2	B86514	hypothetical prote
559	63	6.9	1683	2	AP2071	632	62	6.8	402	2	T12745	hypothetical prote
560	63	6.9	1770	2	S45842	633	62	6.8	408	2	S33683	site-specific DNA
561	63	6.9	1927	2	A59236	634	62	6.8	411	2	S07472	alpha-galactosidas
562	63	6.9	2363	2	T38841	635	62	6.8	415	2	I56481	alpha 1-proteinase
563	63	6.9	4128	2	JC6306	636	62	6.8	415	2	T00140	capsid protein - S
564	63	6.9	6359	2	T31679	637	62	6.8	422	2	AB1154	D-fagatose-bisphos
565	63	6.9	9376	2	T14593	638	62	6.8	427	2	JC4623	prolyl aminopeptid
566	63	6.9	191	2	I37904	639	62	6.8	429	2	T04667	cyclin 2b - Arabid
567	63	6.9	206	1	R3EC4	640	62	6.8	442	2	T39284	nuclear domain 10
568	63	6.9	206	2	A11008	641	62	6.8	446	2	A56733	hypothetical prote
569	63	6.9	206	2	A91149	642	62	6.8	451	2	S43425	tubulin alpha chai
570	63	6.9	206	2	B85994	643	62	6.8	465	2	S74905	hypothetical prote
571	63	6.9	260	1	S28373	644	62	6.8	474	2	A71911	gln-tRNA amidotran
572	63	6.9	260	2	T05559	645	62	6.8	495	2	T14894	glucose-6-phosphat
573	63	6.9	285	2	A95851	646	62	6.8	503	1	O4HUI9	aromatase (EC 1.14
574	63	6.9	301	2	AE1659	647	62	6.8	542	2	AC1704	class I heat-shock
575	63	6.9	302	2	A86898	648	62	6.8	545	2	T52068	RAN GTPase-activat
576	63	6.9	315	2	G91106	649	62	6.8	564	1	KRHUB8	keratin 6b, type I
577	63	6.9	315	2	B85952	650	62	6.8	572	2	AC1880	hypothetical prote
578	63	6.9	316	1	S7EC65	651	62	6.8	577	2	T12536	hypothetical prote
579	63	6.9	342	2	T45069	652	62	6.8	612	2	B84936	RNA polymerase big
580	63	6.9	372	2	G90983	653	62	6.8	617	1	RNUJV7A	transcription init
581	63	6.9	372	2	B85829	654	62	6.8	635	2	T49694	hypothetical prote
582	63	6.9	376	2	T16116	655	62	6.8	660	2	A80893	RNA polymerase big
583	63	6.9	399	2	T38388	656	62	6.8	668	2	B86777	probable anion exc
584	63	6.9	400	1	KRHU9	657	62	6.8	712	2	T02312	hypothetical prote
585	63	6.9	419	2	T51795	658	62	6.8	728	2	T36026	ABC excision nucle
586	63	6.9	445	2	A83078	659	62	6.8	782	2	A34219	Bic-D protein - fir
587	63	6.9	455	2	T23712	660	62	6.8	793	2	S54772	mammary gland fact
588	63	6.9	475	2	G83843	661	62	6.8	833	2	S48558	probable membrane
589	63	6.9	480	2	F71364	662	62	6.8	863	2	AH2286	hypothetical prote
590	63	6.9	480	2	AH1537	663	62	6.8	904	2	G64840	protein-histidine
591	63	6.9	483	2	S41853	664	62	6.8	904	2	D90772	sensor protein for
592	63	6.9	485	2	T32538	665	62	6.8	904	2	H85634	sensor protein for
593	63	6.9	509	2	S66516	666	62	6.8	927	2	T08034	serine/threonine p
594	63	6.9	578	2	D64993	667	62	6.8	980	2	S54986	regulatory protein
595	63	6.9	583	2	A70380	668	62	6.8	987	2	I48373	G-utrophin - mouse
596	63	6.9	591	2	T13650	669	62	6.8	1026	2	S51432	hypothetical prote
597	63	6.9	600	2	T01062	670	62	6.8	1121	2	C82120	transcription regu
598	63	6.9	627	2	T32958	671	62	6.8	1193	2	T12016	hypothetical prote
599	63	6.9	661	2	T51779	672	62	6.8	1218	2	B84537	hypothetical prote
600	63	6.9	744	2	T12705	673	62	6.8	1417	2	F96613	hypothetical prote
601	63	6.9	768	2	T02572	674	62	6.8	1418	2	T37264	phospholipase C (E
602	63	6.9	841	2	T50358	675	62	6.8	1452	2	A97323	DNA polymerase III
603	63	6.9	946	1	A47224	676	62	6.8	1509	1	A27224	myosin heavy chain
604	63	6.9	946	1	A47229	677	62	6.8	1778	2	T50074	probable nucleopor
605	63	6.9	970	2	A36417	678	62	6.8	1790	1	S27772	vitelllogenin precu
606	63	6.9	970	2	S27114	679	62	6.8	1864	2	F66378	protein F219.12 [
607	63	6.9	970	2	I48097	680	62	6.8	1957	2	T38077	hypothetical colle
608	63	6.9	1064	2	H64516	681	62	6.8	2823	2	F79908	protein T22A3.8 [i
609	63	6.9	1068	2	F84614	682	62	6.8	2823	2	T23064	hypothetical prote
610	63	6.9	1503	2	T43166	683	62	6.8	2954	2	T14156	kinase-related pr
611	63	6.9	1959	1	A33977	684	62	6.8	3102	2	T43291	laminin alpha chai
612	63	6.9	1976	2	A59252	685	62	6.8	3433	1	S28381	utrophin - human
613	63	6.9	4464	2	D87755	686	61.5	6.8	155	2	B83771	hypothetical prote

687	61.5	6.8	163	2	S39821	tubulin beta chain	760	61	6.7	435	2	H87516	D-alanyl-D-alanine
688	61.5	6.8	169	2	E91104	probable transcript	761	61	6.7	438	2	A12049	substrate-binding
689	61.5	6.8	169	2	H85919	probable transcript	762	61	6.7	452	2	S47236	ribulose-bisphosph
690	61.5	6.8	242	2	AC2464	hypothetical prote	763	61	6.7	461	2	D72414	anthranilate synth
691	61.5	6.8	269	2	A84841	probable embryo-inh	764	61	6.7	489	1	QJ1289	thiamulokinase (EC
692	61.5	6.8	273	2	T48693	mitochondrial inhe	765	61	6.7	509	2	T12521	hypothetical prote
693	61.5	6.8	306	2	T49541	hypothetical prote	766	61	6.7	517	2	T07704	hypothetical prote
694	61.5	6.8	325	2	T15296	hypothetical prote	767	61	6.7	522	2	J50450	replication initia
695	61.5	6.8	347	2	B72596	hypothetical prote	768	61	6.7	528	2	S73270	chaperonin, 60K -
696	61.5	6.8	352	2	U50637	RegB protein - Thi	769	61	6.7	539	2	T50435	conserved hypotnet
697	61.5	6.8	355	2	A41534	GTP-binding protei	770	61	6.7	540	2	A70358	topoisomerase I -
698	61.5	6.8	406	2	T12171	hypothetical prote	771	61	6.7	562	2	AH2084	hypothetical prote
699	61.5	6.8	425	1	KRX12A	keratin, 64K type	772	61	6.7	591	2	D89783	RBD-containing lip
700	61.5	6.8	426	2	E70058	ubiquitin-cytochro	773	61	6.7	599	2	G83550	GTP-binding protei
701	61.5	6.8	446	2	A41896	transcription acti	774	61	6.7	612	2	AP0079	RNA polymerase sig
702	61.5	6.8	467	2	A49901	NBR1 mobilization	775	61	6.7	615	1	RNEB8T	transcription init
703	61.5	6.8	495	2	AD3038	alpha-amyase amya	776	61	6.7	644	2	B31794	mtm-1 protein (C10
704	61.5	6.8	506	2	G98247	cytoplasmic alpha-	777	61	6.7	676	2	JC7222	77K muscle-derived
705	61.5	6.8	508	2	T40249	hypothetical prote	778	61	6.7	689	2	A31794	mdm-1 nuclear prot
706	61.5	6.8	525	2	G95374	probable ABC trans	779	61	6.7	691	2	F86152	T7123.14 protein -
707	61.5	6.8	537	2	B84772	probable DnaJ prot	780	61	6.7	695	2	JC1493	foliitropin recept
708	61.5	6.8	539	2	S58287	J-domain protein D	781	61	6.7	695	2	G87316	nuclease, probable
709	61.5	6.8	551	2	S67788	hypothetical prote	782	61	6.7	708	2	S53411	hypothetical prote
710	61.5	6.8	566	2	T23926	hemagglutinin-neur	783	61	6.7	794	2	G02317	transcription acti
711	61.5	6.8	571	1	HNN2P2	hemagglutinin-neur	784	61	6.7	805	2	S48411	SSC6 protein - yea
712	61.5	6.8	571	1	HNN2T2	probable two-compo	785	61	6.7	820	2	I48347	protein-lysine k
713	61.5	6.8	588	2	D82958	conserved hypotnet	786	61	6.7	824	2	C86529	glycogen phosphory
714	61.5	6.8	601	2	B81723	hypothetical prote	787	61	6.7	824	2	C72095	phosphorylase (EC
715	61.5	6.8	707	2	T21217	MDH2 dehydrogenas	788	61	6.7	839	2	T39190	probable ATP-depen
716	61.5	6.8	744	2	T13570	endopeptidase La (789	61	6.7	856	1	F64098	endopeptidase Clp
717	61.5	6.8	787	2	A72230	DNA topoisomerase	790	61	6.7	860	2	S76534	hypothetical prote
718	61.5	6.8	806	1	A64078	acetyltransferase	791	61	6.7	882	2	I38912	receptor tyrosine
719	61.5	6.8	846	2	JC7720	flagellar hook-agg	792	61	6.7	886	2	C84517	probable receptor-
720	61.5	6.8	858	2	E72419	serine/threonine-s	793	61	6.7	905	2	T23510	hypothetical comp
721	61.5	6.8	877	2	T01271	sugar hydrolase ho	794	61	6.7	933	2	S49461	synaptonemal compl
722	61.5	6.8	882	2	PC1231	hexokinase (EC 2.7	795	61	6.7	999	2	I38547	novel cellular pro
723	61.5	6.8	882	2	AE1416	hypothetical prote	796	61	6.7	1042	2	A49204	translacion elonga
724	61.5	6.8	924	1	S13913	Na+/Ca2+-exchangin	797	61	6.7	1179	2	G95144	conserved hypotnet
725	61.5	6.8	972	2	C71826	beta-galactosidase	798	61	6.7	1213	2	S42368	hypothetical prote
726	61.5	6.8	973	2	S32815	probable ATPase F2	799	61	6.7	1388	2	T30335	serine/threonine k
727	61.5	6.8	1034	2	T10551	ATP-dependent deox	800	61	6.7	1564	2	S55517	protein H05009.1 [
728	61.5	6.8	1034	2	A24925	insulin receptor-r	801	61	6.7	1648	2	F84833	hypothetical prote
729	61.5	6.8	1123	2	C96622	RNA-directed RNA p	802	61	6.7	1666	2	T43169	probable transcript
730	61.5	6.8	1235	2	AC1728	hypothetical prote	803	61	6.7	1787	2	AC2009	probable SNF2/SW12
731	61.5	6.8	1268	2	B36502	myosin heavy chain	804	61	6.7	2109	2	B89066	hypothetical prote
732	61.5	6.8	1323	1	RRWGM	nonstructural poly	805	61	6.7	2109	2	T33247	serine/threonine k
733	61.5	6.8	1388	2	S70633	cytoplasmic dynein	806	61	6.7	2388	2	JB0271	hypothetical prote
734	61.5	6.8	1391	2	C82007	precortin-2 methyl	807	61	6.7	3187	2	JC5837	beta spectrin, bet
735	61.5	6.8	1445	2	T15212	tyrosine-phosphat	808	61	6.7	149	2	E98191	364K Golgi complex
736	61.5	6.8	1979	1	S03166	MDH2 dehydrogenas	809	60.5	6.7	149	2	AE3095	hypothetical prote
737	61.5	6.8	2514	1	MMW62	coar protein - cas	810	60.5	6.7	178	2	F97325	conserved hypotnet
738	61.5	6.8	4540	2	T10838	MDH2 dehydrogenas	811	60.5	6.7	185	2	A83267	amidease from nicot
739	61	6.7	183	2	H97046	hypothetical prote	812	60.5	6.7	206	2	B97282	probable transcript
740	61	6.7	201	2	B86468	hypothetical prote	813	60.5	6.7	206	2	G81229	ribosomal protein
741	61	6.7	204	2	A33572	uridine-monomorph	814	60.5	6.7	219	2	JQ1075	30S ribosomal prot
742	61	6.7	210	2	B64639	oxygen-Insensitiv	815	60.5	6.7	248	2	F71026	s2 protein - garde
743	61	6.7	219	2	F69341	conserved hypotnet	816	60.5	6.7	258	2	I46080	hypothetical prote
744	61	6.7	244	1	T01091	MDH2 dehydrogenas	817	60.5	6.7	270	2	A34717	uroplakin Ia - bov
745	61	6.7	250	2	G83283	precortin-2 methyl	818	60.5	6.7	279	2	T14332	meiotic recombinat
746	61	6.7	253	2	G70106	tirosine-phosphat	819	60.5	6.7	292	2	T52257	homeotic protein -
747	61	6.7	258	1	VCOMCN	coat protein - cas	820	60.5	6.7	305	2	B72365	CCR4-associated fa
748	61	6.7	260	2	T12427	MDH2 dehydrogenas	821	60.5	6.7	322	2	E69496	porphobilinogen sy
749	61	6.7	287	2	S74050	hypothetical prote	822	60.5	6.7	375	1	C69512	muscone cyclisom
750	61	6.7	326	2	AC1819	hypothetical prote	823	60.5	6.7	376	2	T47519	hypothetical prote
751	61	6.7	345	2	T46962	8-oxoguanine DNA-g	824	60.5	6.7	385	2	A71107	hypothetical prote
752	61	6.7	357	2	A84551	hypothetical prote	825	60.5	6.7	386	2	G88765	protein T11B7.1 [i
753	61	6.7	370	2	H83781	conserved hypotnet	826	60.5	6.7	388	2	T22795	hypothetical prote
754	61	6.7	384	2	H82291	keratin 6d, type I	827	60.5	6.7	403	2	S71356	glucocorticoid-act
755	61	6.7	400	1	ESBOP3	2',3'-cyclic-nucle	828	60.5	6.7	412	2	C91121	tRNA nucleotidyl t
756	61	6.7	411	1	ESBOP3	transposase ISCI31	829	60.5	6.7	426	2	B85966	genome polypotein
757	61	6.7	416	2	T20300	hypothetical prote	830	60.5	6.7	430	2	S28374	ATP-dependent nucl
758	61	6.7	435	2	H75006	methyl-accepting c	831	60.5	6.7	431	2	C64554	hypothetical prote
759	61	6.7	435	2	H75006		832	60.5	6.7	431	2	C71954	

833	60.5	6.7	437	2	T08094	probable sulfate a	906	60	6.6	336	2	S41643	sym protein - Rhi
834	60.5	6.7	445	2	B71642	hypothetical prote	907	60	6.6	335	2	G71804	translacton elonga
835	60.5	6.7	445	2	T24829	hypothetical prote	908	60	6.6	360	2	H71828	probable tRNA (5-m
836	60.5	6.7	449	2	T16891	protein phosphatas	909	60	6.6	360	2	G64686	conserved hypotet
837	60.5	6.7	486	2	H85719	probable oxidoredu	910	60	6.6	360	2	F70045	two-component sens
838	60.5	6.7	486	2	G90897	probable oxidoredu	911	60	6.6	374	2	B89971	conserved hypotet
839	60.5	6.7	496	2	AC1678	carboxy-terminal p	912	60	6.6	384	2	C82385	mannitol-1-phospha
840	60.5	6.7	512	2	C41968	transcription acti	913	60	6.6	394	2	G71528	probable translati
841	60.5	6.7	520	1	G86662	2',3'-cyclic-nucle	914	60	6.6	409	2	T28355	ORF MSV194 Ali mot
842	60.5	6.7	520	2	AG1249	hypothetical prote	915	60	6.6	452	2	S47224	ribose-bisphosph
843	60.5	6.7	520	2	AC1612	hypothetical prote	916	60	6.6	452	2	S47223	glucarate dehydrat
844	60.5	6.7	524	2	A45472	protein kinase (EC	917	60	6.6	455	1	A69753	alpha-galactosidas
845	60.5	6.7	530	2	T42208	propionyl-CoA carb	918	60	6.6	471	2	T01021	hypothetical prote
846	60.5	6.7	544	2	AH1905	hypothetical prote	919	60	6.6	475	2	T32036	hypothetical prote
847	60.5	6.7	545	2	E97728	DNA repair protein	920	60	6.6	491	2	AH0594	probable molybdenu
848	60.5	6.7	578	2	S44975	lmrc protein - Str	921	60	6.6	502	2	S49113	hypothetical prote
849	60.5	6.7	611	2	B85077	probable reverse t	922	60	6.6	515	2	T26210	glucose-6-phosphat
850	60.5	6.7	616	2	D85897	hypothetical prote	923	60	6.6	521	2	T04791	hypothetical prote
851	60.5	6.7	616	2	H91052	molecular chaperon	924	60	6.6	531	2	C70333	hypothetical prote
852	60.5	6.7	616	2	B65029	heat shock cognate	925	60	6.6	589	2	T8905	gamma response 1 p
853	60.5	6.7	624	2	T00044	vacuolar sorting r	926	60	6.6	621	2	S35092	plakoglobin - mous
854	60.5	6.7	628	2	D86466	69.4K hypothetical	927	60	6.6	625	2	T21051	hypothetical prote
855	60.5	6.7	646	2	D82168	two-component hybr	928	60	6.6	645	2	G88130	protein F10G7.4 (i
856	60.5	6.7	650	2	A00352	chaperone protein	929	60	6.6	682	2	F90603	vibrio-like (mycopla
857	60.5	6.7	655	2	F83597	hypothetical prote	930	60	6.6	685	2	A71901	probable flagellar
858	60.5	6.7	687	2	S43250	thimet oligopeptid	931	60	6.6	710	2	AH1109	anaerobic ribonuc
859	60.5	6.7	726	2	A97041	exodeoxyribonuclea	932	60	6.6	714	2	T31819	hypothetical prote
860	60.5	6.7	737	2	AE1678	heavy metal-transp	933	60	6.6	725	2	A47168	cardiac morphogene
861	60.5	6.7	816	2	S54518	probable membrane	934	60	6.6	741	2	T13251	NADH2 dehydrogenas
862	60.5	6.7	835	1	I57441	involucrin - orang	935	60	6.6	745	2	I57655	Sertoli cell leuci
863	60.5	6.7	881	2	T03461	methyl-accepting c	936	60	6.6	757	1	S41712	myb-related protei
864	60.5	6.7	907	1	VGBB7E	glycoprotein B pre	937	60	6.6	881	2	T31739	hypothetical prote
865	60.5	6.7	924	2	C86725	chromosome segrega	938	60	6.6	960	1	S28262	kinesin-related pr
866	60.5	6.7	926	2	D86897	hypothetical prote	939	60	6.6	963	2	T41479	RAD16 nucleotide e
867	60.5	6.7	930	2	T32017	hypothetical prote	940	60	6.6	996	2	AG2366	hypothetical prote
868	60.5	6.7	938	1	SYECIT	isoleucine-tRNA li	941	60	6.6	1036	2	D70117	acetylflavine resist
869	60.5	6.7	967	2	D96573	protein p12M16.21	942	60	6.6	1088	1	P1XRSR	inner layer protei
870	60.5	6.7	1083	2	UC2300	cell surface glyco	943	60	6.6	1178	2	S30431	MSP-300 protein -
871	60.5	6.7	1116	2	D97001	probable membrane	944	60	6.6	1192	2	T84899	receptor-like prot
872	60.5	6.7	1117	2	T14891	telomerase (EC 2.7	945	60	6.6	1237	2	H81660	DNA polymerase III
873	60.5	6.7	1138	2	D85584	probable tail comp	946	60	6.6	1251	2	A56677	neuronal cell cycl
874	60.5	6.7	1162	2	D83454	conserved hypotet	947	60	6.6	1268	2	T31420	C-terminal domain-
875	60.5	6.7	1164	2	T06144	disease resistance	948	60	6.6	1436	2	S57655	probable membrane
876	60.5	6.7	1177	2	A00438	adenomalous polyo	949	60	6.6	1437	2	F69680	DNA-directed DNA p
877	60.5	6.7	1186	2	T23327	ATP-dependent deox	950	60	6.6	1582	2	AC1153	adhesin homolog 1m
878	60.5	6.7	1235	2	AC1358	hypothetical prote	951	60	6.6	1707	2	S77908	hypothetical prote
879	60.5	6.7	1270	2	T26720	hypothetical prote	952	60	6.6	1753	2	T00350	hypothetical prote
880	60.5	6.7	1355	2	S51995	probable ATPase (E	953	60	6.6	1759	2	T18668	myoblast cily prot
881	60.5	6.7	1388	2	S74245	berine/threonine-s	954	60	6.6	1876	2	T28627	vitellogenin - Rip
882	60.5	6.7	1391	2	F81235	DNA-directed RNA p	955	60	6.6	2186	2	T31659	clggrin - fruit fl
883	60.5	6.7	1440	2	JC6312	protein-tyrosine-p	956	60	6.6	2207	2	T42759	Munc13-3 protein -
884	60.5	6.7	1498	2	S78102	chitin synthase (E	957	60	6.6	2434	2	S44861	DNA topoisomerase
885	60.5	6.7	1650	2	S28721	hypothetical prote	958	60	6.6	3329	2	T42205	breast cancer susc
886	60.5	6.7	1759	2	T03725	replisase polyprot	959	60	6.6	3587	2	T31075	tyrocidine synthet
887	60.5	6.7	2151	1	S16449	genome polyprotein	960	59.5	6.6	76	2	F90062	conserved hypotet
888	60.5	6.7	2297	2	AB2494	hypothetical prote	961	59.5	6.6	123	2	D86407	hypothetical prote
889	60.5	6.7	3078	2	T28432	variant-specific b	962	59.5	6.6	175	2	AD1800	transcription regu
890	60.5	6.7	3335	2	H81702	adherens factor T	963	59.5	6.6	201	2	G87641	transcription regu
891	60.5	6.7	3519	2	S43048	polyketide synthas	964	59.5	6.6	228	2	D87488	ABC transporter. A
892	60.5	6.7	3519	2	D36950	uref protein - Bac	965	59.5	6.6	241	2	B69484	hypothetical prote
893	60.5	6.6	148	2	A71876	probable aldehyde	966	59.5	6.6	245	2	G64471	cell division prot
894	60.5	6.6	216	2	U01076	S3 protein - garde	967	59.5	6.6	262	1	A13172	granzyme A (EC 3.4
895	60.5	6.6	219	2	D88990	protein C36C5.12 l	968	59.5	6.6	279	2	G86406	unknown protein (i
896	60.5	6.6	224	2	B84363	H+-transporting AT	969	59.5	6.6	288	2	C86687	hypothetical prote
897	60.5	6.6	234	2	C75552	hypothetical prote	970	59.5	6.6	291	2	S75791	hypothetical prote
898	60.5	6.6	234	2	A84515	probable MADS-box	971	59.5	6.6	293	2	G70444	hypothetical prote
899	60.5	6.6	260	2	T12443	NADH2 dehydrogenas	972	59.5	6.6	324	2	A80554	probable oxidoredu
900	60.5	6.6	260	2	T12431	NADH2 dehydrogenas	973	59.5	6.6	335	2	C64380	porphobilinogen by
901	60.5	6.6	260	2	T12429	NADH2 dehydrogenas	974	59.5	6.6	368	2	T20182	hypothetical prote
902	60.5	6.6	261	2	AF1939	hypothetical prote	975	59.5	6.6	369	1	ESBYPC	3',5'-cyclic-nucle
903	60.5	6.6	262	2	E70365	geranylgeranyl pyr	976	59.5	6.6	378	2	A44443	basic helix-loop-h
904	60.5	6.6	276	2	D70618	hypothetical prote	977	59.5	6.6	397	2	S66700	probable membrane
905	60.5	6.6	277	2	S75803	hypothetical prote	978	59.5	6.6	400	2	B88769	protein C53B4.7 (i

979	59.5	6.6	404	2	A64151	hypothetical prote	1052	59.5	6.6	1951	2	B43963	RNA viral polymera
980	59.5	6.6	412	1	KRSU1	keratin_48k type	1053	59.5	6.6	2116	2	A26555	myosin heavy chain
981	59.5	6.6	419	2	D45045	phycobiliprotein h	1054	59.5	6.6	2150	2	S13553	hypothetical prote
982	59.5	6.6	437	1	S73806	cysteine-tRNA lliga	1055	59.5	6.6	2253	2	T30336	nuclear/mitotic ap
983	59.5	6.6	437	2	UC1165	site-specific DNA-	1056	59.5	6.6	2512	1	MNWS	nonstructural poly
984	59.5	6.6	438	2	T47861	nucleolar autoanti	1057	59.5	6.6	2663	1	S28261	centromere protein
985	59.5	6.6	441	2	T32021	hypothetical prote	1058	59.5	6.6	2747	2	B49132	fat facets (faf) a
986	59.5	6.6	459	2	AB9863	argininosuccinate	1059	59.5	6.6	2829	2	A42771	reticulocyte-bind
987	59.5	6.6	459	2	T31608	hypothetical prote	1060	59.5	6.6	4687	1	A39638	plectin - rat
988	59.5	6.6	464	2	H83752	glutamate dehydrog	1061	59	6.5	144	2	T14170	1-aminocyclopropan
989	59.5	6.6	475	1	B64602	Pet112-like protei	1062	59	6.5	199	2	D70466	ribosomal protein
990	59.5	6.6	493	2	S74652	hypothetical prote	1063	59	6.5	203	2	S43222	hypothetical prote
991	59.5	6.6	498	2	AH0952	conserved hypotnet	1064	59	6.5	209	2	S75029	hypothetical prote
992	59.5	6.6	512	2	C91268	transcription acti	1065	59	6.5	216	1	KIBY8	dTMP kinase (EC 2.
993	59.5	6.6	512	2	AB6109	transcription acti	1066	59	6.5	224	2	T17983	hypothetical prote
994	59.5	6.6	530	2	T32031	hypothetical prote	1067	59	6.5	227	2	C29224	GTP-binding protei
995	59.5	6.6	540	2	T50617	hypothetical prote	1068	59	6.5	244	2	B85926	3'-phosphadenosin
996	59.5	6.6	540	2	B97994	DNA primase (EC 2.	1069	59	6.5	244	2	A91081	3'-phosphadenosin
997	59.5	6.6	592	2	H84018	Mg-protoporphyrin	1070	59	6.5	247	1	QQCV81	coat protein - tom
998	59.5	6.6	595	2	T52327	pectinesterase (EC	1071	59	6.5	251	1	QQCV2	coat protein - pot
999	59.5	6.6	595	2	T02183	probable pectinest	1072	59	6.5	254	2	QQCV82	coat protein - equ
1000	59.5	6.6	621	2	S71215	cellulase (EC 3.2.	1073	59	6.5	254	2	T12668	hypothetical prote
1001	59.5	6.6	623	2	C98048	hypothetical prote	1074	59	6.5	260	2	T12428	hypothetical prote
1002	59.5	6.6	649	2	D96914	chemotaxis protein	1075	59	6.5	260	2	T12424	MDH2 dehydrogenas
1003	59.5	6.6	669	2	T16266	hypothetical prote	1076	59	6.5	260	2	F85630	hypothetical prote
1004	59.5	6.6	690	2	S28222	peroxidase (EC 1.1	1077	59	6.5	301	2	A97412	hypothetical prote
1005	59.5	6.6	700	1	A41615	beta-adrenergic-re	1078	59	6.5	315	2	D71525	probable integrase
1006	59.5	6.6	701	2	S62460	hypothetical prote	1079	59	6.5	322	2	S72271	proteoglycan Lb pr
1007	59.5	6.6	718	2	A81122	hypothetical prote	1080	59	6.5	325	2	T36495	hypothetical prote
1008	59.5	6.6	739	2	A26016	lysine decarboxyla	1081	59	6.5	329	2	A11892	hypothetical prote
1009	59.5	6.6	742	2	T32345	MDH2 dehydrogenas	1082	59	6.5	341	2	T41450	hypothetical prote
1010	59.5	6.6	744	2	T12611	MDH2 dehydrogenas	1083	59	6.5	346	2	T37430	hydroxysteroid deh
1011	59.5	6.6	754	2	T13376	MDH2 dehydrogenas	1084	59	6.5	356	1	A42053	gap junction prote
1012	59.5	6.6	754	2	S63231	hypothetical prote	1085	59	6.5	360	2	T17996	hypothetical prote
1013	59.5	6.6	776	2	C69072	anaerobic ribonuc	1086	59	6.5	393	2	T38663	probable transacti
1014	59.5	6.6	779	2	AG1978	hypothetical prote	1087	59	6.5	394	2	UC1420	translation elonga
1015	59.5	6.6	838	2	JC7363	95K retinoblastoma	1088	59	6.5	399	2	C90455	transposase ISCl31
1016	59.5	6.6	845	2	G64342	hypothetical prote	1089	59	6.5	403	2	B90290	transposase ISCl31
1017	59.5	6.6	879	2	A53901	ribonuclease P (EC	1090	59	6.5	405	2	AD2164	hypothetical prote
1018	59.5	6.6	891	2	JC6519	DNA topoisomerase	1091	59	6.5	411	2	C90252	conserved hypotnet
1019	59.5	6.6	899	2	A44879	retinoblastoma pro	1092	59	6.5	413	2	AC2360	hypothetical prote
1020	59.5	6.6	938	2	D85483	isolectine RNA sy	1093	59	6.5	419	2	F72089	hypothetical prote
1021	59.5	6.6	938	2	B90632	isolectine RNA sy	1094	59	6.5	419	2	F86534	hypothetical prote
1022	59.5	6.6	955	2	S44622	C50C3.3 protein -	1095	59	6.5	423	1	UBFYA	tubulin alpha-1 ch
1023	59.5	6.6	985	2	A96777	hypothetical prote	1096	59	6.5	449	2	S02130	tubulin alpha chain
1024	59.5	6.6	986	2	AB2209	two-component sens	1097	59	6.5	449	2	S04474	tubulin alpha-2 ch
1025	59.5	6.6	991	2	T40229	arginyl endopeptid	1098	59	6.5	458	2	G69123	conserved hypotnet
1026	59.5	6.6	1024	2	T34517	kinesin-related pr	1099	59	6.5	458	2	S57605	probable membrane
1027	59.5	6.6	1025	2	B54718	dihydropyrimidine	1100	59	6.5	461	2	B72625	conserved hypotnet
1028	59.5	6.6	1073	1	OYRHUX	heat-stable antero	1101	59	6.5	470	2	S72279	conserved hypotnet
1029	59.5	6.6	1081	2	S66736	transcription acti	1102	59	6.5	472	2	F82807	hemolysin secretio
1030	59.5	6.6	1119	2	T14321	nuclear matrix con	1103	59	6.5	473	2	F82561	ribulose-bisphosph
1031	59.5	6.6	1127	2	T28317	ORF MSV16 hypotne	1104	59	6.5	475	1	RKXHK	ribulose-bisphosph
1032	59.5	6.6	1173	1	A53430	1-phosphatidylinos	1105	59	6.5	475	1	RKSLT	ribulose-bisphosph
1033	59.5	6.6	1198	2	T43484	hypothetical prote	1106	59	6.5	475	1	RKSLN	two-component sens
1034	59.5	6.6	1225	2	A56514	chromokinesin - ch	1107	59	6.5	479	2	AD1263	hypothetical prote
1035	59.5	6.6	1233	2	T30534	chromosome segrega	1108	59	6.5	492	2	T23523	probable alanine a
1036	59.5	6.6	1259	2	HC5233	yeFN protein - Bgc	1109	59	6.5	505	2	T37975	aromatase (EC 1.14
1037	59.5	6.6	1259	2	G86119	hypothetical prote	1110	59	6.5	508	1	A36121	aromatase (EC 1.14
1038	59.5	6.6	1259	2	G91278	hypothetical prote	1111	59	6.5	513	2	S08381	keratin_58k type
1039	59.5	6.6	1276	2	T18526	SREBP cleavage act	1112	59	6.5	534	2	I37942	keratin 4, type II
1040	59.5	6.6	1379	2	S64603	YTA7 protein - Yea	1113	59	6.5	534	2	S60205	phosphonacetaldoh
1041	59.5	6.6	1401	2	T30247	Werner syndrome pr	1114	59	6.5	554	2	B82934	hypothetical prote
1042	59.5	6.6	1415	2	C86438	hypothetical prote	1115	59	6.5	571	1	D86164	hypothetical prote
1043	59.5	6.6	1481	2	H83017	glutamate synthase	1116	59	6.5	591	1	SBYKT	lysine-tRNA ligase
1044	59.5	6.6	1514	2	S70099	hypothetical prote	1117	59	6.5	592	2	G35115	hypothetical prote
1045	59.5	6.6	1526	2	S49763	gingipain R (EC 3.	1118	59	6.5	620	1	F86269	hypothetical prote
1046	59.5	6.6	1679	2	S49802	probable membrane	1119	59	6.5	621	1	S73825	hypothetical prote
1047	59.5	6.6	1704	2	A55426	gingipain R (EC 3.	1120	59	6.5	623	2	S67762	hypothetical prote
1048	59.5	6.6	1742	2	T49451	kinesin-like prote	1121	59	6.5	639	2	B86587	DNA helicase limpo
1049	59.5	6.6	1893	1	A40262	transcription init	1122	59	6.5	639	2	G72038	ATP-dependent heli
1050	59.5	6.6	1906	1	S68235	myosin-light-chain	1123	59	6.5	642	2	T41690	conserved hypotnet
1051	59.5	6.6	1908	2	A86311	protein FIL3.14 [1	1124	59	6.5	647	2	C83012	probable chemotaxi

1125	59	6.5	654	2	B56011	transcription fact	1198	58.5	6.4	404	2	T19480	hypothetical prote
1126	59	6.5	672	2	C72404	glycine-tRNA ligase	1199	58.5	6.4	409	2	B59433	conserved hypotnet
1127	59	6.5	692	2	T41240	hypothetical zinc	1200	58.5	6.4	413	2	T26072	hypothetical prote
1128	59	6.5	695	2	T45896	follicle stimulat	1201	58.5	6.4	415	1	O4PSCP	camphor 5-monooxyg
1129	59	6.5	741	2	T12762	NADH2 dehydrogenas	1202	58.5	6.4	431	2	T26071	hypothetical prote
1130	59	6.5	743	2	T13700	NADH2 dehydrogenas	1203	58.5	6.4	458	2	G83997	exodeoxyribonuclea
1131	59	6.5	758	2	F72363	hypothetical prote	1204	58.5	6.4	458	2	S57914	probable sakacin P
1132	59	6.5	759	1	B60008	RNA-directed RNA p	1205	58.5	6.4	458	2	S56816	GTPase-activating
1133	59	6.5	759	1	P31V68	RNA-directed RNA p	1206	58.5	6.4	468	2	UC4285	acid phosphatase (
1134	59	6.5	759	2	G86781	5-methyltetrahydro	1207	58.5	6.4	468	2	S55695	suppressor of fuse
1135	59	6.5	762	2	A96634	probable GCNA-comp	1208	58.5	6.4	474	2	B69470	lipase homolog - A
1136	59	6.5	790	2	E48327	COI intron A prote	1209	58.5	6.4	479	1	IXBE1F	alpha trans-induci
1137	59	6.5	814	2	T00740	hypothetical prote	1210	58.5	6.4	481	2	C72377	hypothetical prote
1138	59	6.5	826	2	T23072	hypothetical prote	1211	58.5	6.4	486	2	A64909	probable fructuron
1139	59	6.5	835	2	S40140	hypothetical prote	1212	58.5	6.4	489	1	S66088	conserved hypotnet
1140	59	6.5	860	2	AB2044	ribonucleoside-dip	1213	58.5	6.4	489	2	F97118	levanucrase (limpo
1141	59	6.5	868	2	A84518	adenylate cyclase	1214	58.5	6.4	490	1	IXBE17	alpha trans-induci
1142	59	6.5	887	2	B96598	probable receptor-	1215	58.5	6.4	490	2	I41293	EcoE type I restri
1143	59	6.5	890	1	A53743	hypothetical prote	1216	58.5	6.4	497	2	C70454	transcription regu
1144	59	6.5	897	2	S02032	protein-tyrosine k	1217	58.5	6.4	505	2	B31047	testosterone 16alp
1145	59	6.5	931	2	H96527	alpha-actinin 2, s	1218	58.5	6.4	505	1	S13744	glucose-6-phosphat
1146	59	6.5	944	2	S26710	protein F27015.16	1219	58.5	6.4	508	2	I53018	steroid 17 alpha-h
1147	59	6.5	971	2	T09210	spindle pole body	1220	58.5	6.4	508	2	S52756	steroid 17alpha-mo
1148	59	6.5	996	2	T47518	serine/threonine p	1221	58.5	6.4	512	2	S70644	annexin VII - Afri
1149	59	6.5	1075	1	OYRTX	heat-stable entero	1222	58.5	6.4	516	2	T52611	glucose-6-phosphat
1150	59	6.5	1076	2	UC2217	major surface glyco	1223	58.5	6.4	522	2	T18657	hypothetical prote
1151	59	6.5	1117	2	A38227	RNA-splicing regul	1224	58.5	6.4	522	2	D96602	nucleolar protein
1152	59	6.5	1174	1	A43736	creatine kinase (E	1225	58.5	6.4	529	2	G70140	oligopeptidase ABC t
1153	59	6.5	1331	1	XORTDH	xanthine dehydroge	1226	58.5	6.4	530	2	B96616	hypothetical prote
1154	59	6.5	1335	1	XOWSDH	xanthine dehydroge	1227	58.5	6.4	560	2	B64600	soluble lytic mure
1155	59	6.5	1348	2	B23496	Tyb protein - yeas	1228	58.5	6.4	569	1	S62851	hypothetical prote
1156	59	6.5	1435	2	S59384	hypothetical prote	1229	58.5	6.4	570	2	A48836	filiporellin C prec
1157	59	6.5	1458	2	A45665	adult-specific Bru	1230	58.5	6.4	578	2	T21345	hypothetical prote
1158	59	6.5	1493	2	S49777	probable membrane	1231	58.5	6.4	581	2	B72221	hypothetical prote
1159	59	6.5	1496	2	T05634	hypothetical prote	1232	58.5	6.4	591	2	T51996	hypothetical prote
1160	59	6.5	1660	2	A84647	hypothetical prote	1233	58.5	6.4	591	2	T41531	activator of Hsp70
1161	59	6.5	1679	2	S48385	hypothetical prote	1234	58.5	6.4	624	1	BHTE	hemocyanin chain e
1162	59	6.5	1735	2	A57607	Munc13-1 - rat	1235	58.5	6.4	688	2	T13708	hypothetical prote
1163	59	6.5	1770	2	S58651	Tyb protein - yeas	1236	58.5	6.4	709	2	S03812	hypothetical prote
1164	59	6.5	1770	2	S69966	Tyb protein - yeas	1237	58.5	6.4	714	2	AP2458	exonuclease ABC c
1165	59	6.5	1771	2	S53592	Tyb protein - yeas	1238	58.5	6.4	717	1	S29923	transforming prote
1166	59	6.5	1780	2	T17272	transcription fact	1239	58.5	6.4	717	2	T33295	hypothetical prote
1167	59	6.5	2109	2	I38414	spectrin beta-g ch	1240	58.5	6.4	746	2	T13678	NMDH2 dehydrogenas
1168	59	6.5	2364	1	A44159	splicing factor PR	1241	58.5	6.4	758	2	AB0167	ATP-dependent Clp
1169	59	6.5	2413	2	S34670	centrosome associa	1242	58.5	6.4	778	2	F95188	cation-transportin
1170	59	6.5	2442	2	T08621	hypothetical prote	1243	58.5	6.4	782	2	G98054	P-type ATPase, met
1171	59	6.4	136	2	T13419	hypothetical prote	1244	58.5	6.4	810	2	C70791	probable beta-gala
1172	58.5	6.4	150	2	H83774	hypothetical prote	1245	58.5	6.4	839	2	C84685	transforming prote
1173	58.5	6.4	180	2	G90185	DNA-directed RNA p	1246	58.5	6.4	844	1	TYMSVY	regulatory protei
1174	58.5	6.4	181	2	H87384	acetyltransferase,	1247	58.5	6.4	865	2	A25762	probable membrane
1175	58.5	6.4	206	2	B83113	30S ribosomal prot	1248	58.5	6.4	871	2	S68482	probable carrier p
1176	58.5	6.4	206	2	B82061	ribosomal protein	1249	58.5	6.4	902	1	S54495	cmaA protein - Pse
1177	58.5	6.4	210	2	C70528	hypothetical prote	1250	58.5	6.4	902	2	A55543	hypothetical prote
1178	58.5	6.4	237	2	H64363	hypothetical prote	1251	58.5	6.4	913	1	A41109	protein-tyrosine-p
1179	58.5	6.4	241	2	F71558	probable tRNA pseu	1252	58.5	6.4	947	2	T20156	hypothetical prote
1180	58.5	6.4	260	2	S60480	low temperature-in	1253	58.5	6.4	963	2	AF2119	hypothetical prote
1181	58.5	6.4	263	2	T47074	hypothetical prote	1254	58.5	6.4	970	1	OYZM	phosphoenolpyruvat
1182	58.5	6.4	276	2	B83430	cytochrome-c oxida	1255	58.5	6.4	972	1	T39876	hypothetical prote
1183	58.5	6.4	290	1	D47468	hypothetical prote	1256	58.5	6.4	974	2	A49714	protein-tyrosine k
1184	58.5	6.4	290	2	S53904	hypothetical prote	1257	58.5	6.4	993	2	J02169	RNA 1 protein - cu
1185	58.5	6.4	312	2	T00992	hypothetical prote	1258	58.5	6.4	1008	2	F71727	acetylflavin resista
1186	58.5	6.4	315	2	AC2537	chromosome partiti	1259	58.5	6.4	1032	1	G7BP74	baeoplate protein
1187	58.5	6.4	336	2	H72618	hypothetical prote	1260	58.5	6.4	1034	2	T35054	beta-galactosidase
1188	58.5	6.4	336	2	C84870	probable splicing	1261	58.5	6.4	1035	2	I58409	integrin alpha-9 c
1189	58.5	6.4	365	2	D97848	hypothetical prote	1262	58.5	6.4	1049	1	S51784	toxoin III - Actino
1190	58.5	6.4	370	1	B71937	probable membrane-	1263	58.5	6.4	1052	1	B49219	HIV-1 retropepsin
1191	58.5	6.4	377	2	A81991	hypothetical prote	1264	58.5	6.4	1055	1	GMLJST	protein-tyrosine k
1192	58.5	6.4	382	2	T22798	two-component hydr	1265	58.5	6.4	1064	1	S57450	hypothetical prote
1193	58.5	6.4	385	2	AH2200	probable heat shoc	1266	58.5	6.4	1077	2	T01474	hypothetical prote
1194	58.5	6.4	389	2	A85759	probable heat shoc	1267	58.5	6.4	1102	2	T02782	hypothetical prote
1195	58.5	6.4	389	2	E90860	ycjM protein precu	1268	58.5	6.4	1128	2	AH1949	hypothetical prote
1196	58.5	6.4	389	2	C64876	arginase family pr	1269	58.5	6.4	1132	2	T00259	adenylate cyclase
1197	58.5	6.4	394	2	T37520		1270	58.5	6.4	1144	1	A39833	

1271	58.5	6.4	1188	2	F64367	pyruvate, water di	1344	58	6.4	498	2	T23525	hypothetical prote
1272	58.5	6.4	1273	2	T34558	hypothetical prote	1345	58	6.4	511	2	T27716	hypothetical prote
1273	58.5	6.4	1274	2	T02636	DI protein homolog	1346	58	6.4	530	2	A35114	hypothetical prote
1274	58.5	6.4	1300	2	T18364	ro-3 protein - Neu	1347	58	6.4	530	2	T41865	G64/67 EFP or f128
1275	58.5	6.4	1319	2	S75705	hypothetical prote	1348	58	6.4	538	2	T27156	hypothetical prote
1276	58.5	6.4	1313	2	T20718	hypothetical prote	1349	58	6.4	550	2	T86127	hypothetical prote
1277	58.5	6.4	1353	2	JC4279	adenylate cyclase	1350	58	6.4	550	2	B91286	hypothetical prote
1278	58.5	6.4	1475	2	T33318	hypothetical prote	1351	58	6.4	551	2	C84549	probable membrane
1279	58.5	6.4	1501	2	S57198	multidrug resistan	1352	58	6.4	573	2	S49266	beta-fructofuranos
1280	58.5	6.4	1608	2	T17201	adenylate cyclase	1353	58	6.4	576	2	C86893	cell division regu
1281	58.5	6.4	1711	1	A47392	chromodomain-helic	1354	58	6.4	577	2	T47838	beta-glucosidase-1
1282	58.5	6.4	1932	2	T25525	hypothetical prote	1355	58	6.4	581	2	T38864	probable regulator
1283	58.5	6.4	2541	2	S11661	calin - mouse	1356	58	6.4	585	1	A24168	involucrin - human
1284	58	6.4	154	2	B71263	hypothetical prote	1357	58	6.4	588	2	T48009	PECTINESTERASE-lik
1285	58	6.4	155	2	AD2524	hypothetical prote	1358	58	6.4	594	2	T04545	protein c8/ch-42,
1286	58	6.4	172	2	A80293	hypothetical prote	1359	58	6.4	607	2	E70165	hypothetical prote
1287	58	6.4	178	2	F83664	transcription anti	1360	58	6.4	608	2	A72213	1-deoxyxylulose-5-
1288	58	6.4	206	2	T14330	homeotic protein -	1361	58	6.4	608	2	D87912	protein B0205.3 [i
1289	58	6.4	207	2	D72215	hypothetical prote	1362	58	6.4	615	2	T15575	hypothetical prote
1290	58	6.4	228	2	T47847	hypothetical prote	1363	58	6.4	635	2	F90551	lipoprotein (impor
1291	58	6.4	253	2	E69098	phosphate transpor	1364	58	6.4	647	1	I58353	LIM protein kinase
1292	58	6.4	258	2	S25622	coat protein - cas	1365	58	6.4	653	2	D84286	3-hydroxyacyl-CoA
1293	58	6.4	258	2	S25623	coat protein - cas	1366	58	6.4	663	2	B70460	exonuclease ABC c
1294	58	6.4	260	2	T12446	NADH2 dehydrogenas	1367	58	6.4	686	2	G85940	type III secretion
1295	58	6.4	260	2	T12441	NADH2 dehydrogenas	1368	58	6.4	686	2	C91095	type III secretion
1296	58	6.4	260	2	T12447	NADH2 dehydrogenas	1369	58	6.4	695	1	ORHUP7	follicleotropin recept
1297	58	6.4	260	2	T12432	NADH2 dehydrogenas	1370	58	6.4	705	2	T20278	hypothetical prote
1298	58	6.4	261	2	S52609	hypothetical prote	1371	58	6.4	714	2	H82242	phosphate acetyltr
1299	58	6.4	264	2	F71466	hypothetical prote	1372	58	6.4	723	2	A49613	enoyl-CoA hydratase
1299	58	6.4	264	2	F71466	hypothetical prote	1373	58	6.4	741	2	T13776	NADH2 dehydrogenas
1300	58	6.4	266	2	I49114	Ly49H - mouse	1374	58	6.4	741	2	T12422	NADH2 dehydrogenas
1301	58	6.4	266	2	I49051	Ly-49F-GF antigen	1375	58	6.4	741	2	T13247	NADH2 dehydrogenas
1302	58	6.4	266	2	A70345	hypothetical prote	1376	58	6.4	752	1	KXR1C1	propionin convert
1303	58	6.4	277	2	AD3358	2-dehydro-3-deoxy-	1377	58	6.4	757	2	T38124	hypothetical prote
1304	58	6.4	284	2	C64527	M protein - Helico	1378	58	6.4	759	1	F31V61	RNA-directed RNA p
1305	58	6.4	291	2	T13619	hypothetical prote	1378	58	6.4	759	1	P31VAK	RNA-directed RNA p
1306	58	6.4	298	2	S50735	beta-lactamase (EC	1379	58	6.4	759	1	S04930	RNA-directed RNA p
1307	58	6.4	307	1	PNBSL	hypothetical prote	1380	58	6.4	777	2	C85065	kinesin-like prote
1308	58	6.4	313	2	F70333	hypothetical prote	1381	58	6.4	784	2	F90547	hypothetical prote
1309	58	6.4	317	2	A10640	flagellar hook-ss	1382	58	6.4	784	2	F90547	hypothetical prote
1310	58	6.4	317	2	S10362	hook-associated pr	1383	58	6.4	784	2	A10513	organic solvent to
1311	58	6.4	318	2	A55556	mitogen-activated pr	1384	58	6.4	820	2	T22172	hypothetical prote
1312	58	6.4	322	1	F64360	conserved hypotnet	1385	58	6.4	830	2	E83031	conserved hypotnet
1313	58	6.4	328	2	H84548	hypothetical prote	1386	58	6.4	847	1	A53800	mixed-lineage prot
1314	58	6.4	333	2	D85068	D123-like protein	1387	58	6.4	849	2	T19878	hypothetical prote
1315	58	6.4	342	2	B83272	conserved hypotnet	1388	58	6.4	860	2	T15778	hypothetical prote
1316	58	6.4	345	2	T02650	hypothetical prote	1389	58	6.4	889	2	B70119	preprotein translo
1317	58	6.4	361	2	T21740	hypothetical prote	1390	58	6.4	922	2	T20277	hypothetical prote
1318	58	6.4	361	2	T23732	hypothetical prote	1391	58	6.4	926	2	H88226	protein G41C4.5 [i
1319	58	6.4	368	2	D70481	glucosyl transfera	1392	58	6.4	927	2	T47827	equimosa promoter
1320	58	6.4	371	2	A44122	alpha-helical coil	1393	58	6.4	966	2	F84582	hypothetical prote
1321	58	6.4	373	2	S65176	hypothetical prote	1394	58	6.4	975	2	I59422	reac8 - rat (fmgm
1322	58	6.4	381	2	G83050	L-lactate dehydrog	1395	58	6.4	978	2	G75516	maltoooligosyltreha
1323	58	6.4	384	2	T51423	lycopen dehydrogen	1396	58	6.4	989	2	T15576	hypothetical prote
1324	58	6.4	386	2	S52981	lycopen cyclase -	1397	58	6.4	1029	2	H96658	hypothetical prote
1325	58	6.4	395	2	C90328	transposase ISC131	1398	58	6.4	1030	2	A32612	spectrin alpha cha
1326	58	6.4	397	2	AC0490	probable Arac-fam1	1399	58	6.4	1039	2	S18199	myosin heavy chain
1327	58	6.4	402	2	E70656	hypothetical prote	1400	58	6.4	1061	2	A57620	steroid receptor c
1328	58	6.4	406	2	A43485	argininosuccinate	1401	58	6.4	1089	2	T30883	serine-repeat anti
1329	58	6.4	414	2	S31261	TYA protein - yeas	1402	58	6.4	1101	2	AB2481	hypothetical prote
1330	58	6.4	445	2	F97855	hypothetical prote	1403	58	6.4	1159	1	A44280	inner layer protei
1331	58	6.4	447	2	F85356	hypothetical prote	1404	58	6.4	1194	2	T37503	probable chromosom
1332	58	6.4	448	2	A83775	hypothetical prote	1405	58	6.4	1231	1	A48490	endo-1,4-beta-xyla
1333	58	6.4	451	2	G82218	sensor histidine k	1406	58	6.4	1261	2	S75130	sensory transducti
1334	58	6.4	456	2	G81408	probable outer mem	1407	58	6.4	1300	2	A36502	insulin receptor-r
1335	58	6.4	461	2	B95887	probable aminotran	1408	58	6.4	1354	2	T28107	hypothetical prote
1336	58	6.4	463	2	T10015	hypothetical prote	1409	58	6.4	1354	2	T113930	tripeptidyl-peptid
1337	58	6.4	464	2	T15161	hypothetical prote	1410	58	6.4	1371	2	T29019	hypothetical prote
1338	58	6.4	475	1	RKCNTU	ribulose-bisphosph	1411	58	6.4	1463	2	C86482	protein F5J5.1 [im
1339	58	6.4	484	2	S35401	M1.1 protein precu	1412	58	6.4	1475	2	F86399	protein P17L21.22
1340	58	6.4	484	2	S34978	benzaldehyde denyd	1413	58	6.4	1565	2	S53933	probable membrane
1341	58	6.4	487	2	T71707	conserved hypotnet	1414	58	6.4	1612	2	S53969	DNA topoisomerase
1342	58	6.4	488	2	F86911	conserved hypotnet	1415	58	6.4	1626	2	A39242	DNA topoisomerase
1343	58	6.4	493	2	T31794	hypothetical prote	1416	58	6.4	1803	2	S56894	TYB protein - yeas

1417	58	6.4	1937	2	I38055	myosin heavy chain
1418	58	6.4	1939	1	A46762	myosin alpha heavy
1419	58	6.4	1939	2	D97316	probable S-layer p
1420	58	6.4	1932	2	T43214	ov1 protein - nem
1421	58	6.4	2091	2	A97077	hypothetical prote
1422	58	6.4	2427	2	T16613	hypothetical prote
1423	58	6.4	2925	2	T00133	RNA-directed RNA p
1424	58	6.4	3144	2	A46068	Huntington disease
1425	58	6.4	3746	1	YGPLV3	alpha-aminoadipyl-
1426	58	6.4	3791	1	YGPLV8	alpha-aminoadipyl-
1427	58	6.4	4056	2	H96599	protein F14J16.10
1428	58	6.4	4351	2	T00252	MEGF1 protein - ra
1429	58	6.4	4869	2	S66572	ryanodine receptor
1430	58	6.4	4967	2	S72269	ryanodine receptor
1431	57.5	6.3	148	1	GGHFG3	globin I1 - Atlan
1432	57.5	6.3	151	1	B26092	myosin I2 catalyti
1433	57.5	6.3	179	2	T22301	hypothetical prote
1434	57.5	6.3	190	2	F97301	specialized sigma
1435	57.5	6.3	201	2	B88431	protein M88.2 [imp
1436	57.5	6.3	205	2	B46177	enhancer of split
1437	57.5	6.3	210	2	AH0234	probable two-compo
1438	57.5	6.3	210	2	T47033	hypothetical prote
1439	57.5	6.3	210	2	B81788	conserved hypotet
1440	57.5	6.3	210	2	F90593	lipoprotein [limpor
1441	57.5	6.3	211	2	E90174	superoxide dismuta
1442	57.5	6.3	215	2	E72020	inorganic pyrophos
1443	57.5	6.3	215	2	D86605	inorganic pyrophos
1444	57.5	6.3	216	2	F84023	transcription regu
1445	57.5	6.3	226	2	AD1290	ABC transporter, A
1446	57.5	6.3	228	2	H11682	hypothetical prote
1447	57.5	6.3	235	2	T47432	hypothetical prote
1448	57.5	6.3	239	2	C82870	hypothetical prote
1449	57.5	6.3	245	2	D11554	probable adenylate
1450	57.5	6.3	248	2	T26412	hypothetical prote
1451	57.5	6.3	258	2	AF0499	probable phosphat
1452	57.5	6.3	265	2	T24841	hypothetical prote
1453	57.5	6.3	275	2	S55978	hypothetical prote
1454	57.5	6.3	278	2	G82370	shikimate 5-dehydr
1455	57.5	6.3	282	1	F65061	hypothetical prote
1456	57.5	6.3	292	2	T34529	hypothetical prote
1457	57.5	6.3	293	2	D82557	ABC transporter su
1458	57.5	6.3	301	2	S57531	transcription regu
1459	57.5	6.3	309	2	F83044	nitrate-inducible
1460	57.5	6.3	310	2	B64441	GMP synthase (gluc
1461	57.5	6.3	316	2	A12423	hypothetical prote
1462	57.5	6.3	318	2	F87650	hypothetical prote
1463	57.5	6.3	327	2	T33541	hypothetical prote
1464	57.5	6.3	331	2	T05428	hypothetical prote
1465	57.5	6.3	342	2	T06222	fat-enyl-pyrophosp
1466	57.5	6.3	347	2	AC2456	hypothetical prote
1467	57.5	6.3	349	2	S40718	hypothetical prote
1468	57.5	6.3	352	1	CEBEPX	cell division prot
1469	57.5	6.3	352	2	G91167	cell division memb
1470	57.5	6.3	352	2	G86013	cell division memb
1471	57.5	6.3	354	2	A11976	hypothetical prote
1472	57.5	6.3	359	2	B84674	hypothetical prote
1473	57.5	6.3	360	2	T45649	hypothetical prote
1474	57.5	6.3	364	2	G71410	probable protein k
1475	57.5	6.3	365	2	T04718	hypothetical prote
1476	57.5	6.3	367	2	H85160	hypothetical prote
1477	57.5	6.3	375	2	T40554	rap60 protein - Ba
1478	57.5	6.3	376	2	T49255	protein kinase-lik
1479	57.5	6.3	380	2	UJ0053	UDPGlucose-hexose
1480	57.5	6.3	382	2	A37253	seum albumin - bu
1481	57.5	6.3	394	2	T19571	hypothetical prote
1482	57.5	6.3	401	2	F86754	probable p12 prote
1483	57.5	6.3	408	1	A31888	ribonucleoprotein
1484	57.5	6.3	413	2	AC0882	cRNA adenylatrans
1485	57.5	6.3	427	2	G55259	peptidase, M16 fam
1486	57.5	6.3	427	2	B98125	conserved hypotet
1487	57.5	6.3	428	1	I64227	cysteine-cRNA ligase
1488	57.5	6.3	433	2	T02655	hydroxymethylgluta
1489	57.5	6.3	433	2	B69115	coenzyme F330 synt

1490	57.5	6.3	437	2	S46613	26S proteasome reg
1491	57.5	6.3	440	2	C34332	glutelin 3 precurs
1492	57.5	6.3	444	2	A99496	hypothetical prote
1493	57.5	6.3	445	2	B83805	hypothetical prote
1494	57.5	6.3	455	2	D95923	probable OMA fam1
1495	57.5	6.3	457	2	S52206	mealy protein - leu
1496	57.5	6.3	458	2	B69528	cobalamin acid a,c
1497	57.5	6.3	459	2	T39473	probable geranylge
1498	57.5	6.3	460	2	A83454	oxygen-independent
1499	57.5	6.3	463	2	B55508	interferon alpha I
1500	57.5	6.3	469	2	F82232	indole-3-glycerol

ALIGNMENTS

RESULT 1

JS0204
 trophoblast interferon alpha precursor - sheep
 N/Alternate names: antiluteolytic, trophoblast antiluteolytic protein; trophoblastic pro
 C/Species: Ovis orientalis aries, Ovis aries (domestic sheep)
 C/Date: 31-Mar-1990 #sequence revision 31-Mar-1990 #text change 09-Jul-2004
 C/Accession: S03799; B61403; JS0204; A60947; A53867; S06221; S00306; A60857; A60936
 R/Stewart, H.J.; Flint, A.P.F.; Lamming, G.E.; McCann, S.H.E.; Parkinson, T.J.
 submitted to the EMBL Data Library, June 1988
 A/Reference number: S03799
 A/Accession: S03799
 A/Molecule type: DNA
 A/Residues: 1-195 <STE>
 A/Cross-references: UNIPROT:P56828; UNIPROT:P56829; EMBL:X07920; NID:g1821; PIDN:CA03075
 R/Charlier, M.; Hue, D.; Boismard, M.; Martal, J.; Gaye, P.
 Mol. Cell. Endocrinol. 76, 161-171, 1991
 A/Title: Cloning and structural analysis of two distinct families of ovine interferon- α
 A/Reference number: A61403; MUID:92324492; PMID:1820971
 A/Accession: B61403
 A/Status: not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 1-129, 'K', 131-195 <CHA>
 R/Charlier, M.; Hue, D.; Martal, J.; Gaye, P.
 Gene 77, 341-348, 1989
 A/Title: Cloning and expression of cDNA encoding ovine trophoblastin: its identity with
 A/Reference number: JS0204; MUID:89326151; PMID:2753362
 A/Accession: JS0204
 A/Molecule type: mRNA
 A/Residues: 1-195 <CHM>
 A/Cross-references: GB:M26386; NID:g530199; PIDN:AAA31584.1; PID:g530200
 A/Experimental source: embryo
 R/Stewart, H.J.; McCann, S.H.E.; Northrop, A.J.; Lamming, G.E.; Flint, A.P.F.
 J. Mol. Endocrinol. 2, 65-70, 1989
 A/Title: Sheep antiluteolytic interferon: cDNA sequence and analysis of mRNA levels.
 A/Reference number: A60947; MUID:89351557; PMID:2475129
 A/Accession: A60947
 A/Molecule type: mRNA
 A/Residues: 1-195 <SR3>
 R/Stewart, H.J.; Flint, A.P.F.; Lamming, G.E.; McCann, S.H.E.; Parkinson, T.J.
 J. Reprod. Fert. Suppl. 37, 127-138, 1989
 A/Title: Antiluteolytic effects of blastocyst-secreted interferon investigated in vitro
 A/Reference number: A53867; MUID:90040431; PMID:2530342
 A/Accession: A53867
 A/Molecule type: mRNA
 A/Residues: 1-195 <ST4>
 R/Imakawa, K.; Anthony, R.V.; Kazemi, M.; Marrocci, K.R.; Polites, H.G.; Roberts, R.M.
 Nature 330, 377-379, 1987
 A/Title: Interferon-like sequence of ovine trophoblast protein secreted by embryonic tro
 A/Reference number: S06221; MUID:88065855; PMID:2446135
 A/Accession: S06221
 A/Molecule type: mRNA
 A/Residues: 1-27, 'RK', 30-105, 'E', 107-195 <IMA>
 A/Cross-references: GB:Y00287; NID:g1357; PIDN:CA06836.1; PID:g1358
 R/Charligny, G.; Reinaud, P.; Hue, J.C.; Guillemot, M.; Charlier, M.; Pernollet, J.C.;
 FEBS Lett. 228, 12-16, 1988
 A/Title: High homology between a trophoblastic protein (trophoblastin) isolated from ovi
 A/Reference number: S00306; MUID:88137579; PMID:3254170

Db 84 LQGSFNLFTYTHSSAAMDITLLDQCTGLQOQDLHDTCRGVNGEEDSELGNMDDPIVTV 143

Qy 121 KKYFQGIYDYLQEKGYSDCAMEIVREVMRALTSTTLQKRLTKMGDLNSP 172

Db 144 KKYFQGIYDYLQEKGYSDCAMEIVREVMRALTSTTLQKRLTKMGDLNSP 195

RESULT 5

A:1578 trophoblast protein 1 (clone SPW49) - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 17-Mar-1999

C:Accession: A61578

R:MacKinnon, S.P.; Jeacock, M.K.; Savva, D.; Shepherd, D.A.L.

Int. J. Biochem. 23, 1013-1018, 1991

A:Title: Ovine trophoblast protein-one: evidence for possible glycosylation.

A:Reference number: A61578; MUID:92155417; PMID:1786844

A:Accession: A61578

A:Molecule type: mRNA

A:Residues: 1-172 <MAT>

C:Superfamily: Interferon alpha

F:76/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 93.4%; Score 847; DB 2; Length 172;

Best Local Similarity 93.0%; Pred. No. 2.2e-70;

Matches 160; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CYLSRKMLDARENKLLDRMNRSLPSHSCLODRKDFGLPQEMVEGDQLQKQAFVLYEM 60

Db 1 CYLSRKMLDARENKLLDRMNRSLPSHSCLODRKDFGLPQEMVEGDQLQKQAFVLYEM 60

Qy 61 LQGSFNLFTYTHSSAAMDITLLDQCTGLQOQDLHDTCRGVNGEEDSELGNMDDPIVTV 120

Db 61 LQGSFNLFTYTHSSAAMDITLLDQCTGLQOQDLHDTCRGVNGEEDSELGNMDDPIVTV 120

Qy 121 KKYFQGIYDYLQEKGYSDCAMEIVREVMRALTSTTLQKRLTKMGDLNSP 172

Db 121 KKYFQGIYDYLQEKGYSDCAMEIVREVMRALTSTTLQKRLTKMGDLNSP 172

RESULT 6

A:146272 trophoblast interferon - goat

C:Species: Capra aegagrus hircus (domestic goat)

C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004

C:Accession: I46272

R:Leaman, D.W.; Roberts, R.M.

J. Interferon Res. 12, 1-11, 1992

A:Title: Gene for the trophoblast interferons in sheep, goat, and musk ox and distribut

A:Reference number: I46272; MUID:92242937; PMID:1374107

A:Accession: I46272

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-195 <LEA>

A:Cross-references: UNIPROT:P28171; GB:M73243; NID:G164116; PIDN:AAA30907.1; PID:G164117

C:GeneticB:

A:Gene: CTP-1

C:Superfamily: Interferon alpha

Query Match 93.3%; Score 846; DB 2; Length 195;

Best Local Similarity 93.6%; Pred. No. 3.2e-70;

Matches 161; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CYLSRKMLDARENKLLDRMNRSLPSHSCLODRKDFGLPQEMVEGDQLQKQAFVLYEM 60

Db 24 CYLSRKMLDARENKLLDRMNRSLPSHSCLODRKDFGLPQEMVEGDQLQKQAFVLYEM 83

Qy 61 LQGSFNLFTYTHSSAAMDITLLDQCTGLQOQDLHDTCRGVNGEEDSELGNMDDPIVTV 120

Db 84 LQGSFNLFTYTHSSAAMDITLLDQCTGLQOQDLHDTCRGVNGEEDSELGNMDDPIVTV 143

Qy 121 KKYFQGIYDYLQEKGYSDCAMEIVREVMRALTSTTLQKRLTKMGDLNSP 172

Db 144 KKYFQGIYDYLQEKGYSDCAMEIVREVMRALTSTTLQKRLTKMGDLNSP 195

RESULT 7

A:1455 trophoblast protein 1 precursor - sheep

N:Alternate names: Interferon

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004

C:Accession: A61455; S12624

R:Roberts, R.M.; Cross, J.C.; Farid, C.E.; Hansen, T.R.; Klemann, S.W.; Imakawa, K.

J. Reprod. Fert. Suppl. 41, 63-74, 1990

A:Title: Interferons at the placental interface.

A:Reference number: A61455; MUID:91012357; PMID:2213717

A:Accession: A61455

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-195 <ROB>

A:Cross-references: UNIPROT:Q29429

R:Klemann, S.W.; Imakawa, K.; Roberts, R.M.

Nucleic Acids Res. 18, 6724, 1990

A:Title: Sequence variability among ovine trophoblast interferon cDNA.

A:Reference number: S12624; MUID:91067497; PMID:1701245

A:Accession: S12624

A:Status: preliminary

A:Residues: 1-195 <KLE>

A:Cross-references: EMBL:X56343; NID:G1155013; PIDN:CAA39783.1; PID:G1155014

A:Experimental source: clone cnp-1 p6

C:Superfamily: Interferon alpha

F:1-23/Domains: signal sequence #status predicted <Sig>

F:24-195/Product: trophoblast protein 1 #status predicted <MAT>

Query Match 92.8%; Score 842; DB 2; Length 195;

Best Local Similarity 93.0%; Pred. No. 7.4e-70;

Matches 160; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CYLSRKMLDARENKLLDRMNRSLPSHSCLODRKDFGLPQEMVEGDQLQKQAFVLYEM 60

Db 24 CYLSRKMLDARENKLLDRMNRSLPSHSCLODRKDFGLPQEMVEGDQLQKQAFVLYEM 83

Qy 61 LQGSFNLFTYTHSSAAMDITLLDQCTGLQOQDLHDTCRGVNGEEDSELGNMDDPIVTV 120

Db 84 LQGSFNLFTYTHSSAAMDITLLDQCTGLQOQDLHDTCRGVNGEEDSELGNMDDPIVTV 143

Qy 121 KKYFQGIYDYLQEKGYSDCAMEIVREVMRALTSTTLQKRLTKMGDLNSP 172

Db 144 KKYFQGIYDYLQEKGYSDCAMEIVREVMRALTSTTLQKRLTKMGDLNSP 195

RESULT 8

A:147067 trophoblast protein-1 - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004

C:Accession: I47067

R:Nephew, K.P.; Whaley, A.E.; Christenson, R.K.; Imakawa, K.

Biol. Reprod. 48, 768-778, 1993

A:Title: Differential expression of distinct mRNAs for ovine trophoblast protein-1 and r

A:Reference number: I46387; MUID:93250155; PMID:8465241

A:Accession: I47067

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-195 <NEP>

A:Cross-references: UNIPROT:Q08053; GB:M88770; NID:G165822; PIDN:AAA31504.1; PID:G165823

C:GeneticB:

A:Gene: TP-02

C:Superfamily: Interferon alpha

Query Match 88.9%; Score 806; DB 2; Length 195;

Best Local Similarity 89.5%; Pred. No. 1.5e-66;

Matches 154; Conservative 9; Mismatches 9; Indels 0; Gaps 0;


```
Db 24 CDLSQNHVLFQTKNRLRLLGQMRRLSPFRCLODRKDFAPQEMVWGQLOQAQALSVLHEM 83
Oy 61 LQGSFNLFTYTHSSAAMDITLLLEQLCTGLQOQDLHLDTCRGQVGEEDSBLGNMDPIVTV 120
Db 84 LQGSFNLFTYTHSSAAMDITLLLEQLRTGLHQQLDLDLACLGQVWGEEDSALGRGTPTLAV 143
Oy 121 KKYPQGIYDYLQEKGYSDCAMEIVRVMRALTVTTLQKRLTKMGDLNSP 172
Db 144 KRYFGIHVYLKEKGYSDCAMEIVRVEIMRSLSSSTLSQERLRMMGDVNSP 195

RESULT 17
Interferon omega - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C:Accession: 147070
R:Leaman, D.W.; Roberts, R.M.
J: Interferon Res. 12, 1-11, 1992
A:Title: Genes for the trophoblast interferons in sheep, goat, and musk ox and distribut
A:Reference number: 146272; PMID:92242937; PMID:1374107
A:Accession: 147070
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-195 <LEA>
A:Cross-references: UNIPROT:P28170; GB:M73245; NID:g165828; P1DN:AAA31507.1; PID:g165828
C:Genetic8:
A:Gene: OIFN-omega
C:Superfamily: Interferon alpha

Query Match 64.7%; Score 587; DB 2; Length 195;
Best Local Similarity 67.4%; Pred. No. 1.7e-46;
Matches 116; Conservative 20; Mismatches 36; Indels 0; Gaps 0;

Oy 1 CYLSRKMLDARENLKLLDRMNRSLPHSCLODRKDFGLPQEMVWGQLOQAQAFVLYEM 60
Db 24 CDLSQNHVLFQTKNRLRLLGQMRRLSPFRCLODRKDFAPQEMVWGQLOQAQALSVLHEM 83
Oy 61 LQGSFNLFTYTHSSAAMDITLLLEQLCTGLQOQDLHLDTCRGQVGEEDSBLGNMDPIVTV 120
Db 84 LQGSFNLFTYTHSSAAMDITLLLEQLRTGLHQQLDLDLACLGQVWGEEDSALGRGTPTLAV 143
Oy 121 KKYPQGIYDYLQEKGYSDCAMEIVRVMRALTVTTLQKRLTKMGDLNSP 172
Db 144 KRYFGIHVYLKEKGYSDCAMEIVRVEIMRSLSSSTLSQERLRMMGDVNSP 195

RESULT 18
Interferon alpha - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: 146397
R:Nephew, K.P.; Whaley, A.E.; Christenson, R.K.; Imakawa, K.
BioJ. Reprod. 48, 768-778, 1993
A:Title: Differential expression of distinct mRNAs for ovine trophoblast protein-1 and 2
A:Reference number: 146397; PMID:93250155; PMID:8485241
A:Accession: 146397
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-195 <NEP>
A:Cross-references: UNIPROT:Q28561; EMBL:X59067; NID:g146541; P1DN:CAA41790.1; PID:g4165
C:Genetic8:
A:Gene: Amy 124
C:Superfamily: Interferon alpha

Query Match 64.5%; Score 585; DB 2; Length 195;
Best Local Similarity 66.9%; Pred. No. 2.6e-46;
Matches 115; Conservative 20; Mismatches 37; Indels 0; Gaps 0;

Oy 1 CYLSRKMLDARENLKLLDRMNRSLPHSCLODRKDFGLPQEMVWGQLOQAQAFVLYEM 60
Db 24 CDLSQNHVLFQTKNRLRLLGQMRRLSPFRCLODRKDFAPQEMVWGQLOQAQALSVLHEM 83
```

```
Db 24 CDLSQNHVLFQTKNRLRLLGQMRRLSPFRCLODRKDFAPQEMVWGQLOQAQALSVLHEM 83
Oy 61 LQGSFNLFTYTHSSAAMDITLLLEQLCTGLQOQDLHLDTCRGQVGEEDSBLGNMDPIVTV 120
Db 84 LQGSFNLFTYTHSSAAMDITLLLEQLRTGLHQQLDLDLACLGQVWGEEDSALGRGTPTLAV 143
Oy 121 KKYPQGIYDYLQEKGYSDCAMEIVRVMRALTVTTLQKRLTKMGDLNSP 172
Db 144 KRYFGIHVYLKEKGYSDCAMEIVRVEIMRSLSSSTLSQERLRMMGDVNSP 195

RESULT 19
Interferon alpha-II-1 precursor - bovine
N:Alternate names: BoIFN-alpha-II-1; BoIFN-omega-1
C:Species: Bos primigenius taurus (cattle)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C:Accession: B23285
R:Capon, D.J.; Shepard, H.M.; Goeddel, D.V.
Mol. Cell. Biol. 5, 768-779, 1985
A:Title: Two distinct families of human and bovine interferon-alpha genes are coordinate
A:Reference number: A93070; PMID:65187974; PMID:2985969
A:Accession: B23285
A:Molecule type: DNA
A:Residues: 1-195 <CAP>
A:Cross-references: UNIPROT:P07352; GB:M11002; NID:g163177; P1DN:AAA30578.1; PID:g163178
A:Experimental source: pancreas
C:Comment: Viral infection induces coordinate expression of both alpha-I and alpha-II (on
C:Keywords: antiviral
C:Superfamily: Interferon alpha

Query Match 64.2%; Score 582; DB 1; Length 195;
Best Local Similarity 66.9%; Pred. No. 4.8e-46;
Matches 115; Conservative 18; Mismatches 39; Indels 0; Gaps 0;

Oy 1 CYLSRKMLDARENLKLLDRMNRSLPHSCLODRKDFGLPQEMVWGQLOQAQAFVLYEM 60
Db 24 CDLSQNHVLFQTKNRLRLLGQMRRLSPFRCLODRKDFAPQEMVWGQLOQAQALSVLHEM 83
Oy 61 LQGSFNLFTYTHSSAAMDITLLLEQLCTGLQOQDLHLDTCRGQVGEEDSBLGNMDPIVTV 120
Db 84 LQGSFNLFTYTHSSAAMDITLLLEQLRTGLHQQLDLDLACLGQVWGEEDSALGRGTPTLAV 143
Oy 121 KKYPQGIYDYLQEKGYSDCAMEIVRVMRALTVTTLQKRLTKMGDLNSP 172
Db 144 KRYFGIHVYLQEKGYSDCAMEIVRVEIMRSLSSSTLSQERLRMMGDVNSP 195

RESULT 20
Interferon alpha-II-5 precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S23711
R:Mege, D.; Lefevre, F.; Labonnardiere, C.
J. Interferon Res. 11, 341-350, 1991
A:Title: The porcine family of interferon-omega: cloning, structural analysis, and funct
A:Reference number: S23709; PMID:92193689; PMID:1800582
A:Accession: S23711
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-190 <MEG>
A:Cross-references: UNIPROT:Q29085; EMBL:X57196; NID:g2066; P1DN:CAA40482.1; PID:g2067
C:Superfamily: Interferon alpha

Query Match 56.6%; Score 513.5; DB 2; Length 190;
Best Local Similarity 62.0%; Pred. No. 8.7e-40;
Matches 106; Conservative 24; Mismatches 36; Indels 5; Gaps 1;

Oy 1 CYLSRKMLDARENLKLLDRMNRSLPHSCLODRKDFGLPQEMVWGQLOQAQAFVLYEM 60
Db 24 CDLSQNHVLFQTKNRLRLLGQMRRLSPFRCLODRKDFAPQEMVWGQLOQAQALSVLHEM 83
```


A:Cross-references: GB:V00541; GB:J00213; NID:G32718; PIDN:CAA23802.1; PID:G32719
 A:Note: eight classes of interferon alpha clones were identified; this sequence is derived
 C:Gene: e1ht
 A:Gene: GDB:IFNA5
 A:Cross-references: GDB:136362; OMIM:147565
 A:Map position: 9p22-9p22
 C:Superfamily: interferon alpha
 C:Keywords: antiviral; cytokine; leukocyte
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-189/Product: interferon alpha-5 #status predicted <MAT>

Query Match 48.5%; Score 440; DB 1; Length 189;
 Best Local Similarity 53.0%; Pred. No. 4.7e-33;
 Matches 87; Conservative 28; Mismatches 49; Indels 0; Gaps 0;

Oy 1 CYLSRKMLDARENKILDRMNRSLPHSCLODRKDFGLPOEMVSGDOLQKQAFPVLYEM 60
 Db 24 CDLPQTHSLNRRTMTMAQMGRIISFSCLDKDRHDFGPEEPGNOFQKAQALSVLHEM 83
 Oy 61 LQGSFNLFEYTHSSAAMDITLLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNNDPIVTY 120
 Db 84 IQQTFNLFSTEDSSAAMDITLLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNNDPIVTY 143
 Oy 121 KRYFGIYDYLQEKGYSDCAMEIVRVMRRLTVSTTLQKRLTK 164
 Db 144 RKYFORITLYLTERKYSPCAMEVVRRAEIMRSFSLSANLQERLRR 187

RESULT 31

1VHDA9
 Interferon alpha-17 precursor - human
 N:Alternate names: interferon alpha-9; interferon alpha-I'

C:Date: 01-Sep-1991 #sequence revision 01-Sep-1991 #text_change 09-Jul-2004
 C:Accession: A01835; A22255; C42753
 R:Laan, R.M.; Adelman, J.; Bull, T.J.; Gross, M.; Geeddel, D.; Ullrich, A.
 Science 212, 1159-1162, 1981
 A:Title: DNA sequence of two closely linked human leukocyte interferon genes.
 A:Reference number: A94255; MUID:81201124; PMID:6165082
 A:Accession: A01835
 A:Molecule type: DNA

A:Residues: 1-189 <LNA>
 A:Cross-references: UNIPROT:P01571; GB:J00216; GB:V00532; NID:G32633; PIDN:CAA23793.1; F
 R:Mizoguchi, J.; Pitsha, P.M.; Raj, N.B.K.
 DNA 4, 221-232, 1985

A:Title: Efficient expression in Escherichia coli of two species of human interferon- α
 A:Reference number: A22255; MUID:85229553; PMID:3891272
 A:Accession: A22255

A:Molecule type: mRNA
 A:Residues: 1-56, 'H', 58-189 <MTZ>
 A:Cross-references: GB:M11026; NID:G184612; PIDN:AAA52725.1; PID:G306908
 R:Zoon, K.C.; Miller, D.; Beklier, J.; zur Nedden, D.; Enterline, J.C.; Nguyen, N.Y.; Hu,
 J. Biol. Chem. 267, 15210-15216, 1992
 A:Title: Purification and characterization of multiple components of human lymphoblastoid
 A:Reference number: A42753; MUID:92340576; PMID:1634550
 A:Accession: C42753

A:Molecule type: Protein
 A:Residues: 'X', 25-50, 'XX', 53-56 <ZOO>

C:Gene: e1ht
 A:Gene: GDB:IFNA17
 A:Cross-references: GDB:136358; OMIM:147563
 A:Map position: 9p22-9p22
 C:Superfamily: interferon alpha
 C:Keywords: leukocyte
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-189/Product: interferon alpha-17 #status predicted <MAT>
 F:24-122, 52-162/Disulfide bonds: #status predicted

Query Match 48.3%; Score 438; DB 1; Length 189;
 Best Local Similarity 55.5%; Pred. No. 7.1e-33;
 Matches 91; Conservative 25; Mismatches 46; Indels 0; Gaps 0;

Oy 1 CYLSRKMLDARENKILDRMNRSLPHSCLODRKDFGLPOEMVSGDOLQKQAFPVLYEM 60

Db 24 CDLPQTHSLNRRTMTMAQMGRIISFSCLDKDRHDFGPEEPGNOFQKAQALSVLHEM 83
 Oy 61 LQGSFNLFEYTHSSAAMDITLLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNNDPIVTY 120
 Db 84 IQQTFNLFSTEDSSAAMDITLLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNNDPIVTY 143
 Oy 121 KRYFGIYDYLQEKGYSDCAMEIVRVMRRLTVSTTLQKRLTK 164
 Db 144 RKYFORITLYLTERKYSPCAMEVVRRAEIMRSFSLSANLQERLRR 187

RESULT 32

D25843
 Interferon alpha-G - human
 N:Alternate names: human leukocyte interferon (IFN)

C:Species: Homo sapiens (man)
 C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 15-Jun-1996
 C:Accession: D25843
 R:Ohara, O.; Teraoka, H.
 FEBS Lett. 211, 78-82, 1987
 A:Title: Anomalous behavior of human leukocyte interferon subtypes on polyacrylamide gel
 A:Reference number: A91374; MUID:87105954; PMID:3803589
 A:Accession: D25843
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-167 <OHA>
 C:Superfamily: interferon alpha

Query Match 47.5%; Score 431; DB 2; Length 167;
 Best Local Similarity 53.0%; Pred. No. 2.7e-32;
 Matches 87; Conservative 28; Mismatches 49; Indels 0; Gaps 0;

Oy 1 CYLSRKMLDARENKILDRMNRSLPHSCLODRKDFGLPOEMVSGDOLQKQAFPVLYEM 60
 Db 2 CDLPQTHSLNRRTMTMAQMGRIISFSCLDKDRHDFGPEEPGNOFQKAQALSVLHEM 61
 Oy 61 LQGSFNLFEYTHSSAAMDITLLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNNDPIVTY 120
 Db 62 IQQTFNLFSTEDSSAAMDITLLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNNDPIVTY 121
 Oy 121 KRYFGIYDYLQEKGYSDCAMEIVRVMRRLTVSTTLQKRLTK 164
 Db 122 RKYFORITLYLTERKYSPCAMEVVRRAEIMRSFSLSANLQERLRR 165

RESULT 33

1A6398
 Interferon alpha - sheep
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
 C:Accession: I46398
 R:Whaley, A.E.; Carroll, R.S.; Imakawa, K.
 Gene 106, 281-282, 1991

A:Title: Cloning and analysis of a gene encoding ovine interferon alpha-II.
 A:Reference number: I46398; MUID:92039090; PMID:1937057
 A:Accession: I46398
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-195 <WHA>
 A:Cross-references: UNIPROT:Q28562; EMBL:X59068; NID:G1196; PIDN:CAA41791.1; PID:G1197
 C:Gene: e1ht
 A:Gene: Amy49
 C:Superfamily: interferon alpha

Query Match 47.5%; Score 431; DB 2; Length 195;
 Best Local Similarity 54.3%; Pred. No. 3.3e-32;
 Matches 88; Conservative 23; Mismatches 51; Indels 0; Gaps 0;

Oy 11 AREVLKILDRMNRSLPHSCLODRKDFGLPOEMVSGDOLQKQAFPVLYEM 70
 Db 34 SRSTVLDDMRVSPVLCIKDRRDFGPEEPVNGSQFQKQVSVLHEMLQQLFNLHT 93

Oy 71 EHSSAAMDPTTLEOLCTGLQOOLDLDTCRQVWGEEDSELGNDPIYTKYFGCIYDY 130
 Db 94 ARSSAAMNTTLEELHTLHQQLOGLCTLVQAMGEESVLTADSPITMLKRYFQIRILY 153
 Oy 131 LOEKGYSDCAWEIYVENMRALTSTTLOKRLTKKGGDLNSP 172
 Db 154 LDEKHGSCAMELVMEIRAFSSRADIQESLRSDGDLASP 195

RESULT 34

IVHUA8

Interferon alpha-I-4b precursor - human

N:Alternate names: HuIFN-alpha-I-4b; type I interferon

C:Species: Homo sapiens (man)

C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004

C:Accession: E23753

R:Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.; Kov

J.; Mol. Biol. 185, 227-260, 1985

A:Title: Structural relationship of human interferon alpha genes and pseudogenes.

A:Reference number: A92916; MUID:86037205; PMID:4057246

A:Accession: E23753

A:Molecule type: DNA

A:Residues: 1-189 <HEN>

A:Cross-references: UNIPROT:P05014; GB:X02955; NID:g32656; PIDN:CAA26701.1; PID:g758078

C:GeneticS:

A:Gene: GDB:IFN1@

A:Cross-references: GDB:119328; OMIM:147660

A:Map position: 9p22-9p22

C:Superfamily: Interferon alpha

C:Keywords: antiviral

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-189/Product: Interferon alpha-I-4b #status predicted <MAT>

F:24-122,52-162/Disulfide bonds: #status predicted

Query Match 47.3%; Score 429; DB 1; Length 189;

Best Local Similarity 54.3%; Pred. No. 4,8e-32;

Matches 89; Conservative 25; Mismatches 50; Indels 0; Gaps 0;

Oy 1 CYLSRKMLDARENKILDRNNRSLSPHSCLODRKDFGLPQEMVEGDOLQKQAFVLYEM 60
 Db 24 CDLPQTHSLGNRRALLILQKGRISPHSCLODRHDFRPFEEFQDQFOKQALSVLHEM 83
 Oy 61 LOGSFNLFTTEHSSAAMDPTTLEOLCTGLQOOLDLDTCRQVWGEEDSELGNDPIYTV 120
 Db 84 IQQFNLFTSTEDSSAAMGOSLLEKFTSTLYQQLNDLEACVIOEGVEETPLMNEDSLAV 143
 Oy 121 KKYFGIYDYLOEKGYSDCAWEIYVENMRALTSTTLOKRLTK 164
 Db 144 RKYFORITLYLIERKYSFCAMEVRAEIMRSLSTFSTNLOKRLR 187

RESULT 35

Interferon alpha-5 precursor - human

C:Species: Homo sapiens (man)

C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004

C:Accession: A60937; A01830

R:Bartholomew, C.; Windaas, J.D.

J. Interferon Res. 9, 407-417, 1989

A:Title: Identification of a functional allele of a human interferon-alpha gene previous

A:Reference number: A60937; MUID:89328015; PMID:2526839

A:Accession: A60937

A:Molecule type: DNA

A:Residues: 1-189 <BAR>

A:Cross-references: UNIPROT:P01566

A>Note: This genomic sequence, SMTH11A, encodes a functional allele for alpha interfer

ence and is a pseudogene

R:Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandlish, R.; Seeburg

Nature 290, 20-26, 1981

A:Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.

A:Reference number: A93249; MUID:81148795; PMID:6153083

A:Accession: A01830

A:Molecule type: mRNA

A:Residues: 1-189 <GOE>
 A:Cross-references: GB:V00551; GB:J00209; NID:g32748; PIDN:CAA23812.1; PID:g32749
 A>Note: eight classes of interferon alpha clones were identified; this sequence is deriv
 C:GeneticS:
 A:Gene: GDB:IFNA5
 A:Cross-references: GDB:136362; OMIM:147565
 A:Map position: 9p22-9p22
 C:Superfamily: Interferon alpha
 C:Keywords: Leukocyte
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-189/Product: Interferon alpha-5 #status predicted <MAT>
 F:24-122,52-162/Disulfide bonds: #status predicted

Query Match 47.3%; Score 429; DB 1; Length 189;

Best Local Similarity 54.3%; Pred. No. 4,8e-32;

Matches 89; Conservative 26; Mismatches 49; Indels 0; Gaps 0;

Oy 1 CYLSRKMLDARENKILDRNNRSLSPHSCLODRKDFGLPQEMVEGDOLQKQAFVLYEM 60
 Db 24 CDLPQTHSLGNRRALLILQKGRISPHSCLODRHDFRPFEEFQDQFOKQALSVLHEM 83
 Oy 61 LOGSFNLFTTEHSSAAMDPTTLEOLCTGLQOOLDLDTCRQVWGEEDSELGNDPIYTV 120
 Db 84 IQQFNLFTSTEDSSAAMGOSLLEKFTSTLYQQLNDLEACVIOEGVEETPLMNEDSLAV 143
 Oy 121 KKYFGIYDYLOEKGYSDCAWEIYVENMRALTSTTLOKRLTK 164
 Db 144 RKYFORITLYLIERKYSFCAMEVRAEIMRSLSTFSTNLOKRLR 187

RESULT 36

Interferon alpha-1 precursor - human

N:Alternate names: Interferon alpha-13; Interferon alpha-D; Interferon alpha-I-1

C:Species: Homo sapiens (man)

C:Date: 22-May-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004

C:Accession: C23285; A91467; A93226; A93249; I56213; S43715; S41196; A01826

R:Capon, D.J.; Shepard, H.M.; Goeddel, D.V.

Mol. Cell. Biol. 5, 768-779, 1985

A:Title: Two distinct families of human and bovine interferon-alpha genes are coordinate

A:Reference number: A93070; MUID:85187974; PMID:2985969

A:Accession: C23285

A:Molecule type: DNA

A:Residues: 1-189 <CAP>

A:Cross-references: UNIPROT:P01562

R:Mantel, N.; Schwarzelein, M.; Streuli, M.; Panem, S.; Nagata, S.; Weissmann, C.

Gene 10, 1-10, 1980

A:Title: The nucleotide sequence of a cloned human leukocyte interferon cDNA.

A:Reference number: A91467; MUID:81005094; PMID:6157600

A:Accession: A91467

A:Molecule type: mRNA

A:Residues: 1-189 <MAN>

A:Cross-references: GB:V00537; NID:g32711; PIDN:CAA23798.1; PID:g32712

R:Taniguchi, T.; Mantel, N.; Schwarzelein, M.; Nagata, S.; Muramatsu, M.; Weissmann, C.

Nature 285, 547-549, 1980

A:Title: Human leukocyte and fibroblast interferons are structurally related.

A:Reference number: A93226; MUID:80254543; PMID:6157095

A:Accession: A93226

A:Molecule type: mRNA

A:Residues: 1-189 <MAN>

R:Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandlish, R.; Seeburg

Nature 290, 20-26, 1981

A:Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.

A:Reference number: A93249; MUID:81148795; PMID:6153083

A:Accession: A93249

A:Molecule type: mRNA

A:Residues: 1-136, 'V', 138-189 <GOE>

A:Cross-references: GB:V00538; NID:g32713; PIDN:CAA23799.1; PID:g32714

A>Note: eight classes of interferon alpha clones were identified; this sequence is deriv

R:Weber, H.; Weissmann, C.

Nucleic Acids Res. 11, 5661-5669, 1983

A:Title: Formation of genes coding for hybrid proteins by recombination between related,

A:Reference number: I58213; MUID:83299241; PMID:6310510

A:Accession: I58213
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 24-189 <RES>
A:Cross-references: GB:M29884; NID:G184583; PID:AA52714.1; PID:G386794
R:Hencho, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.; Kov
J. Mol. Biol. 185, 227-260, 1985
A:Title: Structural relationship of human interferon alpha genes and pseudogenes.
A:Reference number: A92916; MUID:86037205; PMID:6057246
A:Accession: S43715
A:Molecule type: DNA
A:Residues: 1-189 <HEN>
A:Cross-references: EMBL:X75934
R:Roelofs, N.
submitted to the EMBL Data Library, December 1993
A:Reference number: S41196
A:Accession: S41196
A:Molecule type: DNA
A:Residues: 1-9, 'A', 11-189 <ROS>
A:Cross-references: EMBL:X75934; NID:G439666; PID:CA53538.1; PID:G439667
C:Genetics:
A:Gene: GDB:IFNA1
A:Cross-references: GDB:136353; OMIM:147660
A:Map position: 9p22-9p22
C:Superfamily: interferon alpha
C:Keywords: antiviral; cytokine; leukocyte
F.1-23/Domain: signal sequence #status predicted <SIG>
F.24-189/Product: interferon alpha-1 #status predicted <MAT>
F.24-122,52-162/Diulide bonds: #status predicted

Query Match 47.2%; Score 428; DB 1; Length 189;
Best Local Similarity 53.9%; Pred. No. 5.9e-32;
Matches 90; Conservative 24; Mismatches 47; Indels 6; Gaps 2;

Qy 1 CYLSRKMLDARENKILDRNRLSPHSCLQDRKDFGLPOEMVSGDQLQKQAPVLYEM 60
Db 24 CDLEPHTSLDNRRLTLMIAQMSRISPSCLMDRHPFGPPEFDGQFOKAPATSVLHEL 83
Qy 61 LQGSFNLFTYEHSSAAMDITLLEQLCTGLQOQLDHLDTCRGQVWGEE--DSEIGNMDPI 117
Db 84 IQQIFNLFTTQSSAAMDIEDLDFCTELTQOQLNDLEAC--VMOEEVGETPLMNDISI 140

Qy 118 VTKYFQGIYDYLQEKGYSDCAMEIYVEMRALTVSTTLQKRLTK 164
Db 141 LAVKVFPRITLVLEKKYSPCAMEVVAEIMRSLSSTNQLERLR 187

RESULT 37
146975
Interferon-omega20 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C:Accession: I46975
R:Charlier, M.; L'Hartidon, R.; Boissard, M.; Martal, J.; Gaye, P.
J. Interferon Res. 13, 313-322, 1993
A:Title: Cloning and structural analysis of four genes encoding interferon-omega in rabb
A:Reference number: I46972; MUID:94132653; PMID:8301151
A:Accession: I46975
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-195 <CHA>
A:Cross-references: UNIPROT:Q28847; GB:S69129; NID:G545145; PID:AA60523.1; PID:G545146
C:Superfamily: interferon alpha

Query Match 47.1%; Score 427; DB 2; Length 195;
Best Local Similarity 54.0%; Pred. No. 7.6e-32;
Matches 87; Conservative 25; Mismatches 49; Indels 0; Gaps 0;

Qy 11 ARENKLIDRMNRLSPHSCLQDRKDFGLPOEMVSGDQLQKQAPVLYEM 70
Db 34 SRKTLVLDDMRKRSVPLCLKDRRDFGFPREVVNSQFOKQTVSLHEMLQOIFNLHT 93
Qy 71 EHSSAAMDITLLEQLCTGLQOQLDHLDTCRGQVWGEEDESLGNMDPIVTKVYFQGIYD 130

Db 94 ARSSAAMNNTLLELHTALHQQQLQGLTCLVQAMGEEDSVLTADSPMLMKRYRIRLY 153
Qy 131 LOEKGYSDCAMEIYVEMRALTVSTTLQKRLTMGGDLNS 171
Db 154 LDEKXSGCAMEIYVEMIRAFSTADQLSRSKDDLAS 194

RESULT 38
146972
Interferon-omega44 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C:Accession: I46972
R:Charlier, M.; L'Hartidon, R.; Boissard, M.; Martal, J.; Gaye, P.
J. Interferon Res. 13, 313-322, 1993
A:Title: Cloning and structural analysis of four genes encoding interferon-omega in rabb
A:Reference number: I46972; MUID:94132653; PMID:8301151
A:Accession: I46972
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-195 <CHA>
A:Cross-references: UNIPROT:Q28843; GB:S68997; NID:G545147; PID:AA60524.1; PID:G545148
C:Superfamily: interferon alpha

Query Match 47.0%; Score 426; DB 2; Length 195;
Best Local Similarity 52.0%; Pred. No. 9.3e-32;
Matches 89; Conservative 25; Mismatches 57; Indels 0; Gaps 0;

Qy 1 CYLSRKMLDARENKILDRNRLSPHSCLQDRKDFGLPOEMVSGDQLQKQAPVLYEM 60
Db 24 CDLPHTSVPLSRKTLVLDDMRKRSVPLCLKDRRDFGFPREVVNSQFOKQTVSLHEM 83
Qy 61 LQGSFNLFTYEHSSAAMDITLLEQLCTGLQOQLDHLDTCRGQVWGEEDESLGNMDPIVTV 120
Db 84 LQOIFNLHTARSSAAMNNTLLELHTALHQQQLQGLTCLVQAMGEEDSVLTADSPMLML 143
Qy 121 KKYFQGIYDYLQEKGYSDCAMEIYVEMRALTVSTTLQKRLTMGGDLNS 171
Db 144 KRYFQIRLTVLEKXSGCAMEIYVEMIRAFSTADQLSRSKDDLAS 194

RESULT 39
152347
Interferon alpha-M1 precursor - human
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I52347
R:Linnane, A.W.; Belharz, M.W.; McMullen, G.L.; Macreadie, I.G.; Murphy, M.; Nisbet, I.J.
Biochem. Int. 8, 725-732, 1984
A:Title: Nucleotide sequence and expression in E. coli of a human interferon-alpha gene
A:Reference number: I52347; MUID:84307815; PMID:6089830
A:Accession: I52347
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-189 <RES>
A:Cross-references: UNIPROT:P05014; GB:M27318; NID:G184617; PID:AA52726.1; PID:G306909
C:Genetics:
A:Gene: IFNA
C:Superfamily: interferon alpha

Query Match 46.9%; Score 425; DB 2; Length 189;
Best Local Similarity 54.3%; Pred. No. 1.1e-31;
Matches 89; Conservative 24; Mismatches 51; Indels 0; Gaps 0;

Qy 1 CYLSRKMLDARENKILDRNRLSPHSCLQDRKDFGLPOEMVSGDQLQKQAPVLYEM 60
Db 24 CDLPQHTSLGNRRRLTLMIAQGRISHPSCLKDRRDFGFPREEDGQFOKAOAISVLHEM 83
Qy 61 LQGSFNLFTYEHSSAAMDITLLEQLCTGLQOQLDHLDTCRGQVWGEEDESLGNMDPIVTV 120
Db 84 IQOIFNLFTEDSSAAMWOSLEKFTSTELTQOQLNDLEACVIOEVGVBETPLMNDISILAV 143

```
QY      121 KKYFGIYDYLQEKGYSDCAMEIVREMMRALTVSTTLQKRLTK 164
        :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
DB      144 RKYFQRITLYLTEKKYSPCAWEVRAEIMRSLSFSTNLQKRLRR 187
```

```

RESULT 40
I46974
Interferon-omega45 - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C/Accession: I46974
R/Character: M.; L'Harridon, R.; Boissard, M.; Martial, J.; Gaye, P.
J. Interferon Res. 13, 313-322, 1993
A/Title: Cloning and structural analysis of four genes encoding interferon-omega in rabbit
A/Reference number: I46972, MUID:94132653, PMID:8301151
A/Accession: I46974
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-195 <CH>
A/Cross-references: UNIPROT:Q28845, GB:IS69000, NID:G545151, PIDN:ACG60326.1, PID:G5451515
C/Superfamily: Interferon alpha

```

[illegible]

RESULT 41
S70011
Interferon type I precursor - sheep
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S70011
R/ILV, L.; Leaman, D.W.; Bixby, J.A.; Roberts, R.M.
Biochim. Biophys. Acta 1294, 55-62, 1996
A/Title: A type I ovine interferon with limited similarity to IFN-alpha, IFN-omega and I
A/Reference number: S70011, MUID:96219886, PMID:8639714
A/Accession: S70011
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-195 <Lit>
A/Cross-references: UNIPROT:Q28545, EMBL:U26254, NID:9829612, PIDD:AA06828.1, PID:98296
A/Superfamily: Interferon alpha

[illegible]

RESULT 42
156313
interferon alpha 21 - human
C|Species: Homo sapiens (man)
C|Date: 02-Jul-1996 #sequence_rev1sion 02-Jul-1996 #text_change 09-Jul-2004
C|Accession: 156313
R|Gron, E.; Berrin, V.M.; Jansone, I.; Teimanis, A.; Vishnevsky, Y.; Apsalons, U.
J. Interferon Res. 4, 609-617, 1984
A|Title: Novel human leukocyte interferon subtype and structural comparison of alpha int
A|Reference number: 156313; M|ID:85056523; P|ID:6548765
A|Accession: 156313
A|Status: preliminary;
A|Molecule type: mRNA
A|Residues: 1-181 <RES>
A|Cross-references: UNIPROT:Q14608; GB:M28586; NID:G184636; P|DN:AAA36041.1; P|D:G306912
C|Gene: GDB: IFNA21
C|Gene: GDB: IFNA21
A|Cross-references: GDB:136360; OMIM:147584
A|Map position: 9p22-9p22
C|Superfamily: interferon alpha

	Query Match	46.4%;	Score 421;	DB 21;	Length 181;	
	Best Local Similarity	52.4%;	Pred. NO. 2.4e-31;			
	Matches	86;	Conservative	27;	Mismatches	51; Indels 0; Gaps 0
QY	1	CYSRLKMLDARENIKLIDRNRLSPHSCLDRDKDFGLPQEWESGDLQKDQAFFVLEYEM	60			
Db	16	CDLPQTSLSGRRALLLAQGGRISPSFCLNDRHDFGPQEELPONGNQKAQASVLHEM	75			
QY	61	LQGSFNLFYTHSSANDFTLLLEQLCTGLQQQLDHLDTCRQGVNGEESLGNDPIYTV	120			
Db	76	IQQFNFLSTSDSATSATWQSILLEKFSTELNQLNDLEACVIOAEVGVEETPLMNVDISILAV	135			
QY	121	KKYFGIYDVLYQEGYSCDAWEIYRVEMRALTYSTTLQKRLTK	164			
Db	136	KKVFQRILTLYLTEKKYSPCAWEIVRAELIMRSFSLSKIFQEKLR	179			

```

RESULT 43
184464
Interferon-alpha-F - human
C:Species: Homo sapiens (man)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: 184464; 137583
R:Gren, B.Y.; Berzih, V.M.; Tsimanis, A.Y.; Apsalon, V.R.; Vishnevskii, Y.I.; Yansone, I.
.A.; Lozna, V.P.; Kasean, V.M.; Efimov, V.A.; Sverdlov, E.D.
Dokl. Biochem. 269, 91-95, 1983
A:Title: A new type of leukocytic interferon.
A:Reference number: 137583
A:Accession: 184464
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-189 <RES>
A:Cross-references: UNIPROT:P01568; GB:M12350; NID:G184598; PIDN:AAA52718.1; PID:G306906
A:Accession: 137583
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-189 <RES>
A:Cross-references: EMBL:X00145; NID:G32724; PIDN:CAA24980.1; PID:G32725
C:Genetics:
A:Gene: IFNA
C:Superfamily: Interferon alpha

Query Match      46.4%; Score 421; DB 2; Length 189;
Best Local Similarity 52.4%; Pred. No. 2,66-31;
Matches 86; Conservative 27; Mismatches 51; Indels 0; Gaps 0;

1 CYLSRLKMDAEBNLTILDRMNRISPSCIQDRKDFGLPOBMVSGDQLQKDAFPVLYEM 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
24 CDLPQTHSGNRRALLILAQMGRIISPSCIKDHNDFPFQPEBFGNGNQKXKALSVLEHM 83
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

61 LQGSRLPYTTEHSSAAMDITLLFQLCTGLQOOQDHLDTCRGQVNGEBSLGNMDFIVTV 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

A:Gene:	IFNA
C:Superfamily:	Interferon alpha
Query Match	46.4%; Score 421; DB 2;
Best Local Similarity	52.4%; Pred. No. 2.6e-31;
Matches	86; Conservative . 27; Mismatches 51; Indels 0; Gaps 0.
DY	1 CYLSRKLMDLRBNULKLLDRNNRLSPHSCLODDRDFGLPQMEWGDDQLXKDQAFFVLYEM 60
Db	24 CDLPQTSLGRRRALILAQMGRIISPFCLCDRDHDGFGRPOEFPGNGQPQAQIAISVLHEM 83
DY	61 LQQSFNLFYTHSSAAMDITTLLEOLCTGLQQOQLDHLDTCRQWGESEELSGNDPIYTV 120

Db 84 IQQFNLFTSKDSATWEOSLERFSTELNQNLDBACVIOEVBGETPLMNVDSILAV 143
QY 121 KKVFQGIYDYLOEKGYSDCAMEIVRVEMMRALTVSTTLQKRLTK 164
Db 144 KKFQRIITLYLTEKKYSPCAMEVVRAEIMRFSLSKIFQERLRR 187

RESULT 44
E25843
Interferon alpha-F - human
N/Alternate names: human leukocyte interferon (IFN)
C/Species: Homo sapiens (man)
C/Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
C/Accession: E25843
R/Ohara, O.; Terakoka, H.
FEBS Lett. 211, 78-82, 1987
A/Title: Anomalous behavior of human leukocyte interferon subtypes on polyacrylamide gel
A/Reference number: A91374; PMID:87105954; PMID:3803589
A/Accession: E25843
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-167 <OH>
A/Cross-references: UNIPROT:Q14608
C/Superfamily: Interferon alpha

Query Match 46.2%; Score 419; DB 2; Length 167;
Best Local Similarity 51.8%; Pred. No. 3.4e-31;
Matches 85; Conservative 26; Mismatches 51; Indels 0; Gaps 0;

QY 1 CYLSRKLMIDARENKILDRMNRSLSPHSCLODRKDFGLPOEMVWGDLQKDAQFPVLYEM 60
Db 2 CDLPQTHSLGNRRALILLAGWGRISPFSCLEKDRHDFGPFQEPFGDNGFQKQAISVLHEM 61

QY 61 LQGSFNLFTYHSSAAMDITLLEQLCTGLQOQLDHLDTCRGVMGEEDESLGNMDPIVTV 120
Db 62 IQQFNLFTSKDSATWEOSLERFSTELNQNLDBACVIOEVBGETPLMNVDSILAV 121

QY 121 KKVFQGIYDYLOEKGYSDCAMEIVRVEMMRALTVSTTLQKRLTK 164
Db 122 KKFQRIITLYLTEKKYSPCAMEVVRAEIMRFSLSKIFQERLRR 185

RESULT 45
IVHUF
Interferon alpha-I-F precursor - human
N/Alternate names: HuIFN-alpha-I-F; LeIF F; type I interferon
C/Species: Homo sapiens (man)
C/Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C/Accession: A01832
R/Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn, R.M.; McCandliss, R.; Seeburg
Nature 290, 20-26, 1981
A/Title: The structure of eight distinct cloned human leukocyte interferon cDNAs.
A/Reference number: A93249; PMID:81148795; PMID:6163083
A/Accession: A01832
A/Molecule type: mRNA
A/Residues: 1-189 <COE>
A/Cross-references: UNIPROT:P01568; GB:V00540; GB:J00212; NID:932716; PIDN:CAA23801.1; F
A/Note: eight classes of interferon alpha clones were identified; this sequence is deriv
C/Genetics:
A/Gene: GDB:IFN1@
A/Cross-references: GDB:119328; OMIM:147660
A/Map position: 9p22-9p22
C/Superfamily: Interferon alpha
C/Keywords: antiviral
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-189/Product: Interferon alpha-I-F #status predicted <MAT>
F:24-122,52-162/Diulfide bonds: #status predicted

Query Match 46.2%; Score 419; DB 1; Length 189;
Best Local Similarity 51.8%; Pred. No. 3.9e-31;
Matches 85; Conservative 26; Mismatches 51; Indels 0; Gaps 0;

QY 1 CYLSRKLMIDARENKILDRMNRSLSPHSCLODRKDFGLPOEMVWGDLQKDAQFPVLYEM 60

Db 24 CDLPQTHSLGNRRALILLAGWGRISPFSCLEKDRHDFGPFQEPFGDNGFQKQAISVLHEM 83
QY 61 LQGSFNLFTYHSSAAMDITLLEQLCTGLQOQLDHLDTCRGVMGEEDESLGNMDPIVTV 120
Db 84 IQQFNLFTSKDSATWEOSLERFSTELNQNLDBACVIOEVBGETPLMNVDSILAV 143

QY 121 KKVFQGIYDYLOEKGYSDCAMEIVRVEMMRALTVSTTLQKRLTK 164
Db 144 KKFQRIITLYLTEKKYSPCAMEVVRAEIMRFSLSKIFQERLRR 187

RESULT 46
IVHOA2
Interferon alpha-I-2 precursor - horse
N/Alternate names: EquIFN-alpha-I-2; type I interferon
C/Species: Equus caballus (domestic horse)
C/Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C/Accession: B24912
R/Himler, A.; Hauptmann, R.; Adolf, G.R.; Sweetly, P.
DNA 5, 345-356, 1986
A/Title: Molecular cloning and expression in Escherichia coli of equine type I interferon
A/Reference number: A90956; PMID:87053170; PMID:3022999
A/Accession: B24912
A/Molecule type: DNA
A/Residues: 1-184 <HM>
A/Cross-references: UNIPROT:P05004; GB:M14541; NID:g164218; PIDN:AAA30950.1; PID:g164221
C/Superfamily: Interferon alpha

Query Match 45.0%; Score 408; DB 1; Length 184;
Best Local Similarity 51.2%; Pred. No. 3.9e-30;
Matches 82; Conservative 26; Mismatches 52; Indels 0; Gaps 0;

QY 1 CYLSRKLMIDARENKILDRMNRSLSPHSCLODRKDFGLPOEMVWGDLQKDAQFPVLYEM 60
Db 24 CDLPQTHSLGNRRALILLAGWGRISPFSCLEKDRHDFGPFQEPFGDNGFQKQAISVLHEM 83

QY 61 LQGSFNLFTYHSSAAMDITLLEQLCTGLQOQLDHLDTCRGVMGEEDESLGNMDPIVTV 120
Db 84 IQQFNLFTSKDSATWEOSLERFSTELNQNLDBACVIOEVBGETPLMNVDSILAV 143

QY 121 KKVFQGIYDYLOEKGYSDCAMEIVRVEMMRALTVSTTLQKRLTK 160
Db 144 RRYFORIALYLOEKKYSPCAMEIVRAEIMRFSLSSTNLQ 183

RESULT 47
F25843
Interferon alpha-J - human
N/Alternate names: human leukocyte interferon (IFN)
C/Species: Homo sapiens (man)
C/Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 15-Jun-1996
C/Accession: F25843
R/Ohara, O.; Terakoka, H.
FEBS Lett. 211, 78-82, 1987
A/Title: Anomalous behavior of human leukocyte interferon subtypes on polyacrylamide gel
A/Reference number: A91374; PMID:87105954; PMID:3803589
A/Accession: F25843
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-167 <OH>
C/Superfamily: Interferon alpha

Query Match 44.7%; Score 405; DB 2; Length 167;
Best Local Similarity 51.8%; Pred. No. 6.4e-30;
Matches 85; Conservative 26; Mismatches 53; Indels 0; Gaps 0;

QY 1 CYLSRKLMIDARENKILDRMNRSLSPHSCLODRKDFGLPOEMVWGDLQKDAQFPVLYEM 60

Db 2 CDLPQTHSLRNRRALLLAQMGRIISPSCLDRHFRFPPEBFDGHOQKQOAIISVHHEM 61
 QY 61 LQGSFNLFTYTHSSAANDTTLLEQLCTGLQOQDLHDTCRQGVNGEEDSELGNMDDPIVTV 120
 Db 62 IQQTFNLFSTEDSSAAWESQSLLEKFSFTELYOQLNDLEACVIOEAVGVEETPLMNEDEFLAV 121
 QY 121 KKYFQGIYDYLQEGKGYSDCAWEIVRVMRRALTVSTTLQKRLTK 164
 Db 122 RKYFQRIITLYLMEKKYSPCAWEIVRAEIMRSPFSSTNLKGLRR 165

RESULT 48

IVHUA0

Interferon alpha-7 precursor - human

N/Alternate names: Interferon alpha-7; Leif J

C/Species: Homo sapiens (man)

C/Date: 18-Aug-1992 #sequence_revision 18-Aug-1992 #text_change 09-Jul-2004

C/Accession: A01831; S43717

R/Unlrich, A.; Gray, A.; Goeddel, D.V.; Dull, T.J.

J. Mol. Biol. 156, 467-486, 1992

A/Title: Nucleotide sequence of a portion of human chromosome 9 containing a leukocyte 1

A/Reference number: A01831; MUID:83010248; PMID:6181262

A/Accession: A01831

A/Molecule type: DNA

A/Residues: 1-189 <URL>

A/Cross-references: UNIPROT:P01567; GB:V00531; NID:932631; PIDN:CAA23792.1; PID:932632;

N/Note: This interferon is derived from a gene referred to as J by the authors

R/Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.; Kov

J. Mol. Biol. 185, 227-260, 1985

A/Title: Structural relationship of human interferon alpha genes and pseudogenes.

A/Reference number: A92916; MUID:86037205; PMID:4057246

A/Accession: S43717

A/Molecule type: DNA

A/Residues: 1-189 <HENS>

A/Cross-references: EMBL:X02960; NID:932665; PIDN:CAA26706.1; PID:9758081

C/Genetics:

A/Gene: GDB:IFNA7

A/Cross-references: GDB:136364; OMIM:147567

A/Map position: 9p22-9p22

C/Superfamily: Interferon alpha

C/Keywords: antiviral; cytokine; leukocyte

F/1-23/Domain: signal sequence #status predicted <SIG>

F/24-189/Product: interferon alpha-7 #status predicted <MAT>

F/24-122,52-162/Dissulfide bonds: #status predicted

Query Match 44.7%; Score 405; DB 1; Length 189;
 Best Local Similarity 51.8%; Pred. No. 7,56-30;
 Matches 85; Conservative 26; Mismatches 53; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENLKLLDRNRLSPHSCLDRKDFGLPQEMVGGDLOKQDAFPVLYEM 60
 Db 24 CDLPQTHSLRNRRALLLAQMGRIISPSCLDRHFRFPPEBFDGHOQKQOAIISVHHEM 83
 QY 61 LQGSFNLFTYTHSSAANDTTLLEQLCTGLQOQDLHDTCRQGVNGEEDSELGNMDDPIVTV 120
 Db 84 IQQTFNLFSTEDSSAAWESQSLLEKFSFTELYOQLNDLEACVIOEAVGVEETPLMNEDEFLAV 143
 QY 121 KKYFQGIYDYLQEGKGYSDCAWEIVRVMRRALTVSTTLQKRLTK 164
 Db 144 RKYFQRIITLYLMEKKYSPCAWEIVRAEIMRSPFSSTNLKGLRR 167

RESULT 49

I53102

Interferon-alpha-7 - human

C/Species: Homo sapiens (man)

C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C/Accession: I53102

R/Cohen, S.; Velan, B.; Grosfeld, H.; Shalita, Z.; Leitner, M.; Shaffer, A.

Dev. Biol. Stand. 60, 111-122, 1985

A/Title: Cloning, expression and biological activity of a new variant of human interferon

A/Reference number: I53102; MUID:86005847; PMID:2995168

A/Accession: I53102

A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-189 <RES>
 A/Cross-references: UNIPROT:P01567; GB:M34913; NID:9184614; PIDN:AAA36039.1; PID:9184615
 C/Superfamily: Interferon alpha

Query Match 44.5%; Score 404; DB 2; Length 189;
 Best Local Similarity 51.8%; Pred. No. 9,36-30;
 Matches 85; Conservative 26; Mismatches 53; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENLKLLDRNRLSPHSCLDRKDFGLPQEMVGGDLOKQDAFPVLYEM 60
 Db 24 CDLPQTHSLRNRRALLLAQMGRIISPSCLDRHFRFPPEBFDGHOQKQOAIISVHHEM 83
 QY 61 LQGSFNLFTYTHSSAANDTTLLEQLCTGLQOQDLHDTCRQGVNGEEDSELGNMDDPIVTV 120
 Db 84 IQQTFNLFSTEDSSAAWESQSLLEKFSFTELYOQLNDLEACVIOEAVGVEETPLMNEDEFLAV 143
 QY 121 KKYFQGIYDYLQEGKGYSDCAWEIVRVMRRALTVSTTLQKRLTK 164
 Db 144 RKYFQRIITLYLMEKKYSPCAWEIVRAEIMRSPFSSTNLKGLRR 167

RESULT 50

IVH0A1

Interferon alpha-1 precursor - horse

N/Alternate names: EglFN-alpha-1; type I interferon

C/Species: Equus caballus (domestic horse)

C/Date: 28-Dec-1997 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004

C/Accession: A24912

R/Himmler, A.; Hauptmann, R.; Adolf, G.R.; Smetly, P.

DNA 5, 345-356, 1986

A/Title: Molecular cloning and expression in Escherichia coli of equine type I interferon

A/Reference number: A90956; MUID:87053170; PMID:3022999

A/Accession: A24912

A/Molecule type: DNA

A/Residues: 1-184 <HIM>

A/Cross-references: UNIPROT:P05003; GB:M14540; NID:9164226; PIDN:AAA30953.1; PID:9164227

C/Superfamily: Interferon alpha

C/Keywords: antiviral

F/1-23/Domain: signal sequence #status predicted <SIG>

F/24-184/Product: interferon alpha-1 #status predicted <MAT>

F/24-122,52-162/Dissulfide bonds: #status predicted

Query Match 44.4%; Score 403; DB 1; Length 184;
 Best Local Similarity 51.3%; Pred. No. 1,16-29;
 Matches 81; Conservative 26; Mismatches 51; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENLKLLDRNRLSPHSCLDRKDFGLPQEMVGGDLOKQDAFPVLYEM 60
 Db 24 CDLPQTHSLRNRRALLLAQMGRIISPSCLDRNDPQPFVFDGNOFRKQOAIISAVHET 83
 QY 61 LQGSFNLFTYTHSSAANDTTLLEQLCTGLQOQDLHDTCRQGVNGEEDSELGNMDDPIVTV 120
 Db 84 IQQTFNLFSTEDSSAAWESQSLLEKFSFTELYOQLNDLEACVIOEAVGVEETPLMNEDEFLAV 143
 QY 121 KKYFQGIYDYLQEGKGYSDCAWEIVRVMRRALTVSTTL 158
 Db 144 RRYFQRIITLYLMEKKYSPCAWEIVRAEIMRSPFSSTNL 181

Search completed: October 5, 2005, 10:38:41
 Job time : 72 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 5, 2005, 10:04:45 ; Search time 178 Seconds

(without alignments)
494.818 Million cell updates/sec

Title: US-10-694-247-2

Perfect score: 907
Sequence: 1 CYLSRKMLDARENLKLLDR.....TVSTTLQKRLTKNGGLNSP 172Scoring table: BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summariesDatabase : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	907	100.0	195	1	INT1_SHEEP
2	900	99.2	195	1	INT2_SHEEP
3	888	97.9	172	1	INT3_SHEEP
4	881	97.1	195	1	INT4_SHEEP
5	880	97.0	195	1	INT7_SHEEP
6	877	96.7	195	1	INT5_SHEEP
7	868	95.7	195	1	INT9_SHEEP
8	865	95.4	195	1	INT8_SHEEP
9	846	93.3	195	1	INT_CAPI
10	842	92.8	195	1	INT6_SHEEP
11	830	91.5	195	2	OGUZ29
12	830	91.5	195	2	OGUZ50
13	816	90.0	172	2	OGRF28
14	806	88.9	195	1	INTA_SHEEP
15	804	88.6	195	1	OGUZ47
16	794	87.5	195	2	OGUZ43
17	786	86.7	195	2	OGUZ42
18	780	86.0	195	1	INT_OVIMO
19	778	85.8	195	1	INTB_SHEEP
20	726	80.0	195	1	INTI_SHEEP
21	721	79.5	172	2	INT2_BOVIN
22	719	79.3	172	2	OGMJ29
23	717	79.1	195	2	OGMYK6
24	707	77.9	172	1	INT3_BOVIN
25	702	77.4	195	2	OGGLT6
26	696	76.7	172	2	OGUDU3
27	693	76.4	195	2	OGGLU5
28	679	74.9	195	1	INT_GIRCA
29	653	72.0	195	1	INT_CEREL
30	609	67.1	195	1	INDI_HUMAN
31	608	67.0	195	2	Q7M2Y7

32	587	64.7	195	2	P28170	P28170 ovis aries
33	585	64.5	195	2	Q28561	Q28561 ovis aries
34	582	64.2	195	1	INOI_BOVIN	P07352 bos taurus
35	531	58.5	129	1	Q6SMQ8	Q6smq8 bos mutus g
36	513.5	56.6	190	2	Q29085	Q29085 sus scrofa
37	499	55.0	195	1	IN02_HORSE	P05002 equus caball
38	488.5	53.9	190	2	Q29098	Q29098 sus scrofa
39	473	52.1	195	1	IN01_HUMAN	P05000 homo sapien
40	469.5	51.8	179	2	Q29084	Q29084 sus scrofa
41	462	50.9	174	2	Q13168	Q13168 homo sapien
42	444	49.0	195	1	IN01_HORSE	P05001 equus caball
43	440	48.5	189	1	IN45_HUMAN	P01569 homo sapien
44	440	48.5	189	1	INAD_HUMAN	P01570 homo sapien
45	438	48.3	189	1	INAG_HUMAN	P01571 homo sapien
46	431	47.5	195	2	Q28562	Q28562 ovis aries
47	430	47.4	195	2	Q28844	Q28844 oryctolagus
48	429	47.3	189	1	IN44_HUMAN	P05014 homo sapien
49	429	47.3	189	1	IN4A_HUMAN	P01566 homo sapien
50	428	47.2	166	2	Q9UMJ3	Q9umj3 homo sapien
51	428	47.2	189	1	IN41_HUMAN	P01562 homo sapien
52	428	47.2	189	2	Q14605	Q14605 homo sapien
53	427	47.1	195	2	Q28847	Q28847 oryctolagus
54	426	47.0	195	2	Q28843	Q28843 oryctolagus
55	425	46.9	189	2	Q95J78	Q95j78 saginus oe
56	424	46.7	195	2	Q28845	Q28845 oryctolagus
57	423	46.6	195	2	Q28545	Q28545 ovis aries
58	421	46.4	181	2	Q14608	Q14608 homo sapien
59	421	46.4	189	1	IN4K_HUMAN	P01568 homo sapien
60	418	46.1	189	2	Q95J77	Q95j77 saginus oe
61	417	46.0	166	2	Q8WZ68	Q8wz68 homo sapien
62	412	45.4	166	2	Q7YRK9	Q7yrk9 sus scrofa
63	408	45.0	184	1	IN42_HORSE	P05004 equus caball
64	405	44.7	189	1	IN47_HUMAN	P01567 homo sapien
65	403	44.4	184	1	IN41_HORSE	P05003 equus caball
66	403	44.4	184	1	IN43_HORSE	P05006 equus caball
67	403	44.4	184	1	IN44_HORSE	Q8mj1 saimiri sci
68	400	44.1	174	2	Q8MT11	Q8mt11 sus scrofa
69	400	44.1	189	2	Q68105	Q68105 sus scrofa
70	399	44.0	189	2	Q6VAB8	Q6vab8 sus scrofa
71	398	43.9	189	1	IN4F_HUMAN	P05015 homo sapien
72	397.5	43.8	166	2	Q86UP4	Q86up4 homo sapien
73	394.5	43.5	188	1	IN42_HUMAN	P01563 homo sapien
74	394	43.4	166	2	P792Z8	P792z8 odocoileus
75	394	43.4	189	2	Q6QTF5	Q6qtf5 sus scrofa
76	392	43.2	189	2	Q14618	Q14618 homo sapien
77	386	42.6	189	1	IN48_HUMAN	P32881 homo sapien
78	384	42.3	189	1	IN41_PIG	P49879 sus scrofa
79	384	42.3	189	1	IN45_MOUSE	P07349 mus musculus
80	384	42.3	189	2	Q81062	Q81062 mus musculus
81	381	42.0	189	2	Q80SU4	Q80su4 mus musculus
82	380	41.9	189	1	Q81067	Q81067 mus musculus
83	380	41.9	190	1	IN49_MOUSE	P09233 mus musculus
84	379	41.8	166	2	Q6HOM6	Q6hom6 bos sp. ifn
85	378	41.7	189	1	IN46_HUMAN	P05013 homo sapien
86	378	41.7	190	2	Q617I9	Q617i9 mus musculus
87	376	41.5	189	1	IN41_BOVIN	P07348 bos taurus
88	375	41.3	189	1	IN41_MOUSE	P01572 mus musculus
89	374	41.2	166	2	Q6HOM5	Q6hom5 bos sp. ifn
90	374	41.2	190	1	IN47_MOUSE	P06799 mus musculus
91	372	41.0	190	1	IN42_MOUSE	P01573 mus musculus
92	371	40.9	166	2	Q7YRF0	Q7yrf0 bos taurus
93	371	40.9	189	1	IN4H_BOVIN	P49878 bos taurus
94	371	40.9	192	1	IN41_RAT	P05011 ratius nov
95	370.5	40.8	154	2	Q6ONB6	Q6onb6 homo sapien
96	370	40.8	189	2	Q810G5	Q810g5 mus musculus
97	368	40.6	189	1	IN4D_BOVIN	P05010 bos taurus
98	368	40.6	201	2	Q8R5K9	Q8r5k9 marmota mon
99	367	40.5	190	2	Q89N22	Q89n22 marmota mon
100	365.5	40.3	188	2	Q86316	Q86316 felis alive
101	365	40.2	190	2	Q8R5J2	Q8r5j2 marmota mon
102	365	40.2	190	2	Q64138	Q64138 cisticinae
103	364	40.1	190	2	Q61716	Q61716 mus musculus
104	364	40.1	190	2	Q61718	Q61718 mus musculus

105	364	40.1	190	2	Q810G4	Q810G4 mus musculus	178	197.5	21.8	182	2	Q810G0	Q810G0 mus musculus
106	363	40.0	190	2	Q8R5J4	Q8R5J4 marmota mon	179	197.5	21.8	182	2	Q8B0T1	Q8B0T1 mus musculus
107	362.5	40.0	188	2	Q8R5J5	Q8R5J5 felis silve	180	192.5	21.2	182	2	Q8C0T3	Q8C0T3 mus musculus
108	362	39.9	189	2	Q80S55	Q80S55 mus musculus	181	180.5	19.9	90	2	Q14645	Q14645 homo sapien
109	362	39.9	189	2	Q8R5V5	Q8R5V5 marmota mon	182	176	19.4	73	2	Q8HYG2	Q8HYG2 macropus eu
110	360	39.7	189	1	INAB_BOVIN	P05008 bos taurus	183	175	19.3	73	2	Q8HYG9	Q8HYG9 macropus eu
111	359	39.6	189	2	Q8MIL7	Q8MIL7 felis silve	184	172.5	19.0	184	1	INB_RAT	P70459 ratus norv
112	359	39.6	189	2	Q8MIL7	Q8MIL7 felis silve	185	170	18.7	73	2	Q8HYG5	Q8HYG5 macropus eu
113	359	39.6	189	2	Q8MIL7	Q8MIL7 felis silve	186	166	18.3	73	2	Q8HYG8	Q8HYG8 macropus eu
114	359	39.6	189	2	Q8MIL7	Q8MIL7 felis silve	187	164	18.1	73	2	Q8HYG6	Q8HYG6 macropus eu
115	359	39.6	189	2	Q8MIL7	Q8MIL7 felis silve	188	164	18.1	182	1	INB_MOUSE	Q8HYG6 macropus eu
116	358	39.5	166	2	Q7YRH8	Q7YRH8 bubalus bub	189	162	17.9	203	1	INFB_CHICK	Q90873 gallus gall
117	358	39.5	166	2	Q7YRH9	Q7YRH9 bubalus bub	190	159	17.5	73	2	Q8HYG7	Q8HYG7 macropus eu
118	358	39.5	189	1	INAF_BOVIN	P49876 bos taurus	191	159	17.5	73	2	Q8HYG8	Q8HYG8 macropus eu
119	358	39.5	189	2	Q8MIL5	Q8MIL5 felis silve	192	157	17.3	180	2	Q70S66	Q70S66 fugu rubrip
120	358	39.5	190	2	Q8R5J3	Q8R5J3 marmota mon	193	156	17.2	180	2	Q63Z66	Q63Z66 fugu rubrip
121	358	39.5	190	2	Q8VHY8	Q8VHY8 marmota mon	194	155.5	17.1	82	2	Q912B3	Q912B3 mus musculus
122	357	39.4	189	1	INAG_BOVIN	Q810G1 mus musculus	195	155	17.1	73	2	Q8HYT4	Q8HYT4 macropus eu
123	357	39.4	191	2	Q810G1	Q810G1 mus musculus	196	151	16.6	73	2	Q8HYG3	Q8HYG3 macropus eu
124	357	39.4	191	2	Q8X1G2	Q8X1G2 mus musculus	197	149	16.4	73	2	Q8HYH3	Q8HYH3 macropus eu
125	356	39.3	189	2	Q8MIL3	Q8MIL3 felis silve	198	147	16.2	73	2	Q8HYF8	Q8HYF8 macropus eu
126	356	39.3	189	2	Q8MIL4	Q8MIL4 felis silve	199	147	16.2	73	2	Q8HYG0	Q8HYG0 macropus eu
127	356	39.3	189	2	Q810G3	Q810G3 mus musculus	200	147	16.2	199	2	Q7TS10	Q7TS10 mus musculus
128	356	39.3	197	2	Q8R5J7	Q8R5J7 marmota mon	201	142	15.7	73	2	Q8HYT0	Q8HYT0 macropus eu
129	356	39.3	197	2	Q8VHZ1	Q8VHZ1 marmota mon	202	140	15.4	73	2	Q8HYH1	Q8HYH1 macropus eu
130	355	39.1	189	1	INAA_BOVIN	P05007 bos taurus	203	138	15.2	73	2	Q8HYH5	Q8HYH5 macropus eu
131	355	39.1	190	2	Q810G6	Q810G6 mus musculus	204	136.5	15.0	191	2	Q60UZ2	Q60UZ2 anser anser
132	355	39.1	190	2	Q9ESJ1	Q9ESJ1 marmota mon	205	134.5	14.8	193	1	INFI_CHICK	P42165 gallus gall
133	354	39.0	166	2	Q7YRL3	Q7YRL3 bos taurus	206	134.5	14.8	193	2	Q9PW16	Q9PW16 gallus gall
134	354	38.8	197	2	Q8VHZ0	Q8VHZ0 marmota mon	207	133.5	14.7	191	1	INF_ANAPL	P51526 anas platyr
135	351	38.7	189	1	INAC_BOVIN	P05009 bos taurus	208	133	14.7	73	2	Q8HYG1	Q8HYG1 macropus eu
136	350	38.6	197	2	Q8VHY9	Q8VHY9 marmota mon	209	133	14.7	73	2	Q8HYH2	Q8HYH2 macropus eu
137	349.5	38.5	194	2	Q8MIL6	Q8MIL6 felis silve	210	130	14.3	73	2	Q8HYH9	Q8HYH9 macropus eu
138	343	37.8	186	2	Q8R5J6	Q8R5J6 marmota mon	211	128.5	14.2	192	1	INF_MELGA	P51527 meleagris g
139	342	37.7	189	1	INAB_MOUSE	P07350 mus musculus	212	127	14.0	73	2	Q8HYH0	Q8HYH0 macropus eu
140	340.5	37.5	194	1	INA_FELCA	P35849 felis silve	213	125.5	13.8	193	2	Q9PW15	Q9PW15 gallus gall
141	340.5	37.5	194	2	Q863J1	Q863J1 felis silve	214	124	13.7	73	2	Q8HYI3	Q8HYI3 macropus eu
142	340	37.5	189	1	INAB_MOUSE	P17660 mus musculus	215	123.5	13.6	193	1	INF3_CHICK	Q90872 gallus gall
143	335	36.9	136	1	Q61717	Q61717 mus musculus	216	123	13.6	73	2	Q8HYF9	Q8HYF9 macropus eu
144	331.5	36.5	186	1	INAA_MOUSE	P07351 mus musculus	217	119.5	13.2	176	2	Q7ZS24	Q7ZS24 tetradon n
145	329	36.3	183	2	Q7YRX8	Q7YRX8 macropus eu	218	113.5	12.5	72	2	Q8HXB0	Q8HXB0 cachygiobsu
146	324	35.7	201	2	Q8R5J1	Q8R5J1 marmota mon	219	111	12.2	175	2	Q6XQ67	Q6XQ67 salmo salar
147	318	35.1	187	1	INAB_CANPA	Q97945 canis fami1	220	110.5	12.2	72	2	Q16055	Q16055 homo sapien
148	317	35.0	187	2	Q867A7	Q867A7 canis fami1	221	110.5	12.2	72	2	Q8HYF5	Q8HYF5 cachygiobsu
149	316	34.8	187	1	INAI_CANPA	P81255 canis fami1	222	109.5	12.1	197	2	Q7SSP9	Q7SSP9 coturnix co
150	316	34.8	187	2	Q7SUT5	Q7SUT5 canis fami1	223	109	12.0	175	2	Q6XQ66	Q6XQ66 salmo salar
151	314	34.6	190	2	Q91WX3	Q91WX3 sigmodon hi	224	107.5	11.9	72	2	Q16054	Q16054 homo sapien
152	313	34.5	187	2	Q7SUL7	Q7SUL7 canis fami1	225	106	11.7	73	2	Q8HYH6	Q8HYH6 macropus eu
153	310	34.2	187	2	Q7YRX7	Q7YRX7 canis fami1	226	104.5	11.5	72	2	Q9UNH4	Q9UNH4 homo sapien
154	301	33.2	183	2	Q7YRX7	Q7YRX7 macropus eu	227	103.5	11.4	68	2	Q8HYH7	Q8HYH7 macropus eu
155	294	32.4	108	2	Q9N1U6	Q9N1U6 equus cabal	228	103	11.4	73	2	Q8HYF3	Q8HYF3 cachygiobsu
156	293	32.3	208	2	Q7TQ91	Q7TQ91 peromyscus	229	103	11.4	73	2	Q8HYF4	Q8HYF4 cachygiobsu
157	290	32.0	208	2	Q86WN2	Q86WN2 homo sapien	230	100	11.0	73	2	Q8HYH4	Q8HYH4 macropus eu
158	287.5	31.7	186	1	INB2_BOVIN	P01576 bos taurus	231	99	10.9	73	2	Q8HYE2	Q8HYE2 cachygiobsu
159	285	31.4	128	2	Q7TQ92	Q7TQ92 peromyscus	232	99	10.9	73	2	Q8HYI5	Q8HYI5 macropus eu
160	266.5	29.4	187	2	Q6XZW6	Q6XZW6 cachygiobsu	233	97	10.7	73	2	Q8HYE6	Q8HYE6 cachygiobsu
161	260	28.7	186	2	Q6B1Q4	Q6B1Q4 sus scrofa	234	97	10.7	73	2	Q8HYE7	Q8HYE7 macropus eu
162	257	28.3	186	1	INB_HORSE	P05012 equus cabal	235	96.5	10.6	133	2	Q701I8	Q701I8 coturnix co
163	257	28.3	186	2	Q294I2	Q294I2 sus scrofa	236	94.5	10.4	68	2	Q8HYI2	Q8HYI2 macropus eu
164	255	28.1	186	1	INB3_BOVIN	P01577 bos taurus	237	94.5	10.4	84	2	Q951B8	Q951B8 sus scrofa
165	254.5	28.1	170	2	Q291I5	Q291I5 sus scrofa	238	90.5	10.0	84	2	Q951B8	Q951B8 sus scrofa
166	254	28.0	182	2	Q6XZW7	Q6XZW7 cachygiobsu	239	90	9.9	1182	2	Q8ID30	Q8ID30 plasmodium
167	253.5	27.9	187	1	INB_HUMAN	P01574 homo sapien	240	89.5	9.9	68	2	Q8HYG4	Q8HYG4 macropus eu
168	253.5	27.9	187	2	Q776I2	Q776I2 macaca fasc	241	87.5	9.6	68	2	Q8HYI1	Q8HYI1 macropus eu
169	251	27.7	186	1	INB_FELCA	Q9N210 felis silve	242	85.5	9.4	2239	2	Q81B8	Q81B8 plasmodium
170	250.5	27.6	170	2	Q291I4	Q291I4 sus scrofa	243	85	9.4	253	2	Q66ZV9	Q66ZV9 boirella ga
171	241.5	26.6	187	2	Q15943	Q15943 homo sapien	244	85	9.4	1920	1	PCT2_MOUSE	P48725 mus musculus
172	235.5	26.0	207	2	Q9P0W0	Q9P0W0 homo sapien	245	84.5	9.3	186	1	ATPF_MESVI	Q9MUI1 mesostigma
173	233	25.7	192	2	Q80ZEF2	Q80ZEF2 mus musculus	246	84	9.3	167	2	Q8EBD1	Q8EBD1 oceanobacil
174	230.5	25.4	186	1	INB1_BOVIN	P01578 bos taurus	247	83	9.2	241	2	Q9M1R0	Q9M1R0 arabidopsis
175	227	25.0	93	2	Q75T05	Q75T05 cyccolagus	248	83	9.2	2838	2	Q8VHU9	Q8VHU9 ratus norv
176	226.5	25.0	183	2	Q7YRX6	Q7YRX6 macropus eu	249	82.5	9.1	297	2	Q9H5C1	Q9H5C1 homo sapien
177	199.5	22.0	182	2	Q9R1T0	Q9R1T0 mus musculus	250	82	9.0	496	2	Q42434	Q42434 notophthalm

251	82	9.0	581	2	06Y5M8	06Y5M8 mus musculus	324	76.5	8.4	854	2	06NUP4	06NUP4 homo sapien
252	82	9.0	805	2	09NCNS	09NCNS euploies ae	325	76.5	8.4	1131	2	08Y143	08Y143 arabidopsis sp
253	82	9.0	1512	2	08CDL2	08CDL2 mus musculus	326	76.5	8.4	1465	2	07TP27	07TP27 rattus norv
254	82	9.0	1911	2	08OU10	08OU10 mus musculus	327	76.5	8.4	1705	2	07REB8	07REB8 plasmidium
255	81.5	9.0	302	2	06X853	06X853 streptococc	328	76	8.4	129	2	095235	095235 plasmidium
256	81.5	9.0	373	2	08VX54	08VX54 solanum tub	329	76	8.4	133	2	0964R4	0964R4 plasmidium
257	81.5	9.0	382	2	06UEHS	06UEHS aspergillus	330	76	8.4	459	2	07SYF7	07SYF7 acipenser b
258	81.5	9.0	412	2	05O371	05O371 methylolphil	331	76	8.4	511	2	08W117	08W117 arabidopsis
259	81.5	9.0	739	2	09M9G4	09M9G4 arabidopsis	332	76	8.4	519	1	YB29-STAN	YB29-STAN staphylococ
260	81.5	9.0	752	2	09A1V6	09A1V6 arabidopsis	333	76	8.4	519	1	YB69-STAM	YB69-STAM staphylococ
261	81.5	9.0	752	2	09A1V6	09A1V6 arabidopsis	334	76	8.4	519	1	YB69-STAM	YB69-STAM staphylococ
262	81.5	9.0	846	2	06NVC9	06NVC9 brachydanio	335	76	8.4	519	2	06G9S7	06G9S7 staphylococ
263	81.5	9.0	8407	2	07RTM4	07RTM4 homo sapien	336	76	8.4	519	2	06GHE9	06GHE9 staphylococ
264	81	8.9	136	2	07OG08	07OG08 oncorhynch	337	76	8.4	573	2	06E1R4	06E1R4 geobacillus
265	81	8.9	180	2	06SR85	06SR85 carassius a	338	76	8.4	573	2	06E1R6	06E1R6 geobacillus
266	81	8.9	309	2	08W1K2	08W1K2 crataegus	339	76	8.4	573	2	06E1R6	06E1R6 geobacillus
267	81	8.9	332	1	NDP2-VIBVY	NDP2-VIBVY vibrio vuln	340	76	8.4	573	2	06E1R7	06E1R7 geobacillus
268	81	8.9	564	2	06C435	06C435 variowia li	341	76	8.4	574	2	0803C5	0803C5 brachydanio
269	81	8.9	873	2	098949	098949 gallus gall	342	76	8.4	605	2	07SYN2	07SYN2 brachydanio
270	81	8.9	2178	2	081643	081643 plasmidium	343	76	8.4	634	2	09PUD1	09PUD1 chlamydia m
271	80.5	8.9	301	2	06D220	06D220 erwina car	344	76	8.4	826	2	08TL94	08TL94 methanosa
272	80.5	8.9	407	2	06LH49	06LH49 photobacter	345	76	8.3	880	2	08QFP9	08QFP9 xenopus lae
273	80.5	8.9	581	1	CN67-YEAST	CN67-YEAST saccharomyc	346	75.5	8.3	187	2	090196	090196 spodoptera
274	80	8.8	350	2	09JMM4	09JMM4 wolbachia s	347	75.5	8.3	208	1	RS4-HAEDU	RS4-HAEDU haemophilus
275	80	8.8	734	2	07OEC6	07OEC6 anopheles g	348	75.5	8.3	227	2	08MTC4	08MTC4 drosophila
276	80	8.8	2042	2	025766	025766 plasmidium	349	75.5	8.3	392	2	06H8K4	06H8K4 porcine par
277	79.5	8.8	344	2	097WC3	097WC3 sulfobobus	350	75.5	8.3	545	2	06DB26	06DB26 erwina car
278	79.5	8.8	378	1	TGT-VIBVU	TGT-VIBVU vibrio vuln	351	75.5	8.3	890	2	09DPS8	09DPS8 saint croix
279	79.5	8.8	379	1	TGT-VIBCH	TGT-VIBCH vibrio chol	352	75.5	8.3	1499	2	07OP68	07OP68 giardia lam
280	79.5	8.8	433	2	07MNH1	07MNH1 vibrio vuln	353	75	8.3	158	2	07NSM2	07NSM2 chromobacte
281	79.5	8.8	804	2	06FYE7	06FYE7 bartonella	354	75	8.3	160	2	07S7E0	07S7E0 neurospora
282	79.5	8.8	927	2	06C1S9	06C1S9 kluyveromyc	355	75	8.3	164	2	087124	087124 neurospora
283	79.5	8.8	2710	2	09XZ88	09XZ88 plasmidium	356	75	8.3	196	2	06LYV9	06LYV9 methanococ
284	79.5	8.8	3026	2	026030	026030 plasmidium	357	75	8.3	461	1	TRME-HELPU	TRME-HELPU helicobacte
285	79	8.7	285	2	073EKS	073EKS bacillus ce	358	75	8.3	502	1	K2C8-XENIA	K2C8-XENIA xenopus lae
286	79	8.7	897	2	06GLI4	06GLI4 variowia li	359	75	8.3	507	2	07ZXU4	07ZXU4 xenopus lae
287	78	8.6	290	2	06LL14	06LL14 photobacter	360	75	8.3	514	2	MR11-MOUSE	MR11-MOUSE mus muscu
288	78	8.6	331	1	RFOA-MOUSU	RFOA-MOUSU wolfinella s	361	75	8.3	573	2	06E1N0	06E1N0 bacillus sp
289	78	8.6	453	2	08BWD3	08BWD3 m mus muscu	362	75	8.3	573	2	06E1N2	06E1N2 bacillus th
290	78	8.6	487	2	061373	061373 drosophila	363	75	8.3	573	2	06E1N3	06E1N3 bacillus th
291	78	8.6	487	2	09VJ06	09VJ06 drosophila	364	75	8.3	573	2	06E1N4	06E1N4 bacillus st
292	78	8.6	488	1	K2C8-MOUSE	K2C8-MOUSE mus muscu	365	75	8.3	573	2	06E1N8	06E1N8 bacillus th
293	78	8.6	502	1	DCE1-ARATH	DCE1-ARATH arabidopsis	366	75	8.3	573	2	06E1N9	06E1N9 bacillus th
294	78	8.6	680	2	08B1F5	08B1F5 m mus muscu	367	75	8.3	1503	1	MUKB-HAEDU	MUKB-HAEDU haemophilus
295	78	8.6	762	2	08BM85	08BM85 m mus muscu	368	75	8.3	1821	2	07X8X4	07X8X4 tyza sativ
296	78	8.6	772	2	092555	092555 homo sapien	369	74.5	8.2	213	1	THAI-HUMAN	THAI-HUMAN homo sapien
297	78	8.6	1141	2	091Y79	091Y79 rattus norv	370	74.5	8.2	332	2	06LX57	06LX57 methanococ
298	78	8.6	1299	2	06GLR7	06GLR7 xenopus lae	371	74.5	8.2	374	1	TGT-YERPE	TGT-YERPE pseudomonas
299	78	8.6	3255	2	09PKM8	09PKM8 chlamydia m	372	74.5	8.2	378	2	066D95	066D95 clostridium
300	77.5	8.5	496	1	WDJ7-MOUSE	WDJ7-MOUSE mus muscu	373	74.5	8.2	378	2	0898G5	0898G5 yersinia pe
301	77.5	8.5	1029	2	059809	059809 schizosacch	374	74.5	8.2	510	2	06C8T5	06C8T5 clostridium
302	77.5	8.5	1495	2	06CS07	06CS07 kluyveromyc	375	74.5	8.2	520	2	06DE01	06DE01 xenopus lae
303	77.5	8.5	1514	2	06BBR6	06BBR6 legionella	376	74.5	8.2	545	2	091B62	091B62 xenopus lae
304	77.5	8.5	247	2	081ZES	081ZES bacillus an	377	74.5	8.2	569	2	09HVN7	09HVN7 pseudomonas
305	77	8.5	247	2	08HP78	08HP78 bacillus th	378	74.5	8.2	657	1	UVRB-BACCA	UVRB-BACCA brachydanio
306	77	8.5	562	2	09Z3J1	09Z3J1 mus muscu	379	74.5	8.2	758	1	GOA1-MOUSE	GOA1-MOUSE mus muscu
307	77	8.5	573	2	06E1N7	06E1N7 bacillus th	380	74.5	8.2	897	2	08ASR6	08ASR6 bacteroides
308	77	8.5	576	1	REC_N-BACSU	REC_N-BACSU bacillus su	381	74.5	8.2	1092	2	06L3H7	06L3H7 solanum dem
309	77	8.5	879	2	096GV6	096GV6 homo sapien	382	74.5	8.2	1162	2	0754X1	0754X1 aabhyra goss
310	77	8.5	879	2	08KKY1	08KKY1 rhizobium e	383	74.5	8.2	1906	2	0813H0	0813H0 plasmidium
311	77	8.5	893	2	08TEA7	08TEA7 homo sapien	384	74.5	8.2	8797	1	SNEI-HUMAN	SNEI-HUMAN homo sapien
312	77	8.5	115	2	059193	059193 pyrococcus	385	74.5	8.2	127	2	08OQT2	08OQT2 equid herpe
313	76.5	8.4	191	2	09H7K0	09H7K0 homo sapien	386	74.5	8.2	220	2	064QR4	064QR4 bacteroides
314	76.5	8.4	213	2	061A39	061A39 homo sapien	387	74	8.2	243	2	06YJ03	06YJ03 onion yello
315	76.5	8.4	230	2	06F9F2	06F9F2 acinetobact	388	74	8.2	295	2	07NIG2	07NIG2 gloeobacter
316	76.5	8.4	287	2	08R2V2	08R2V2 mus muscu	389	74	8.2	382	2	07VLD4	07VLD4 haemophilus
317	76.5	8.4	322	2	06BQC0	06BQC0 debaromyce	390	74	8.2	391	2	099QD7	099QD7 caulobacter
318	76.5	8.4	375	2	06LU69	06LU69 photobacter	391	74	8.2	533	2	06S101	06S101 uncultured
319	76.5	8.4	377	1	TGT-VIBPA	TGT-VIBPA aabhyra goss	392	74	8.2	573	2	06E1P8	06E1P8 geobacillus
320	76.5	8.4	565	2	075CD7	075CD7 aabhyra goss	393	74	8.2	874	2	09Y166	09Y166 brachydanio
321	76.5	8.4	590	2	094287	094287 caenorhabdi	394	74	8.2	1431	2	09NG75	09NG75 paratemia
322	76.5	8.4	651	2	09HFM9	09HFM9 gliomus moss	395	74	8.2				
323	76.5	8.4					396	74	8.2				

397	74	8.2	1802	2	048647	048647 oryza sativ	470	72	7.9	397	2	07PW81	07PW81 anopheles g
398	74	8.2	4041	2	06FMG2	06fmg2 candida gla	467	72	7.9	467	2	09GCV0	09GCV0 triatolepi
399	73.5	8.1	269	2	094238	094238 caenorhadi	472	72	7.9	487	2	061518	061518 mus musculu
400	73.5	8.1	312	2	08BVN7	08bvnt mus musculi	473	72	7.9	490	2	061463	061463 mus musculu
401	73.5	8.1	367	2	061PP6	061ppe homo sapien	474	72	7.9	509	2	08HUG6	08HUG6 sesbania ve
402	73.5	8.1	375	2	095PO5	095ppo moligula ocu	475	72	7.9	517	2	08T768	08T768 brachiocto
403	73.5	8.1	435	1	SNXR_HUMAN	096192 homo sapien	476	72	7.9	598	2	09LU94	09LU94 arabidopsis
404	73.5	8.1	446	2	08VX56	08vx56 solanum tub	477	72	7.9	601	2	06TLH1	06TLH1 brachydanio
405	73.5	8.1	478	2	086632	086632 beet crypti	478	72	7.9	674	2	09K1S8	09K1S8 chlamydia p
406	73.5	8.1	519	2	080T21	080t21 mus musculu	479	72	7.9	680	2	09Z7B0	09Z7B0 chlamydia p
407	73.5	8.1	532	2	07TOL6	07tql6 mus musculu	480	72	7.9	745	2	073KR5	073KR5 treponema d
408	73.5	8.1	549	1	TBC3_HUMAN	081zpt1 homo sapien	481	72	7.9	758	2	044893	044893 caenorhadi
409	73.5	8.1	549	2	061PX1	061px1 homo sapien	482	72	7.9	796	2	049464	049464 arabidopsis
410	73.5	8.1	704	2	09U2J3	08u2j3 caenorhadi	483	72	7.9	868	2	09BG31	09BG31 rhizobium 1
411	73.5	8.1	813	1	PEPX_LACPL	088y02 lactobacilli	484	72	7.9	1066	1	SYI_PYRFU	P66214 pyrococcus
412	73.5	8.1	817	2	09BUI1	09bj11 caenorhadi	485	72	7.9	1471	2	07QF02	07QF02 giardia lam
413	73.5	8.1	894	2	08EG31	08egb1 shewanella	486	72	7.9	1851	2	09ESP3	09esp3 rattus norv
414	73.5	8.1	984	2	093HT8	093ht8 clostridium	487	72	7.9	2215	2	086D77	086d77 varroa dest
415	73.5	8.1	1034	2	06LX78	06lx78 methanococc	488	72	7.9	4589	2	076506	076506 tetrahymena
416	73.5	8.1	1149	2	09P8H7	09p8h7 candida alb	489	72	7.9	4924	2	09P7T1	09P7T1 echinosacch
417	73.5	8.1	1956	2	09Y2K3	09y2k3 homo sapien	490	72	7.9	158	2	075S22	075s22 brachydanio
418	73	8.0	265	2	06MQS7	06mqst mus musculu	491	71.5	7.9	179	2	0800H1	0800h1 brachydanio
419	73	8.0	341	1	TAFF_MOUSE	091lc0 mus musculu	492	71.5	7.9	183	2	0800G9	0800g9 brachydanio
420	73	8.0	360	2	07Q896	07q896 anopheles g	493	71.5	7.9	185	2	08AY12	08ay12 brachydanio
421	73	8.0	408	2	06C0L6	06c0l6 yarrowia li	494	71.5	7.9	217	2	09VYR0	09vy10 dtrosophila
422	73	8.0	472	2	06D3Q2	06d3q2 erwina car	495	71.5	7.9	269	2	06Z248	06z248 oryza sativ
423	73	8.0	484	2	09QVZ4	09qyz4 mus musculu	496	71.5	7.9	353	2	09S832	09sb32 arabidopsis
424	73	8.0	493	2	015872	015872 paramecium	497	71.5	7.9	375	1	TGT_SALTY	08zic8 salinonella
425	73	8.0	493	2	08L9X0	08l9x0 arabidopsis	498	71.5	7.9	431	2	09V587	09v587 dtrosophila
426	73	8.0	517	2	06K5H5	06k5h5 oryza sativ	499	71.5	7.9	421	2	08T320	08t320 dtrosophila
427	73	8.0	519	2	061G01	061g01 rattus norv	500	71.5	7.9	434	2	08BOK5	08bqk5 mus musculu
428	73	8.0	534	2	09CAB0	09cab0 arabidopsis	501	71.5	7.9	494	2	08ENM2	08enm2 oceanobacil
429	73	8.0	553	2	09Z332	09z332 mus musculu	502	71.5	7.9	522	2	09C9T9	09c9t9 arabidopsis
430	73	8.0	622	2	Q7YU54	Q7yu54 dtrosophila	503	71.5	7.9	549	2	06DHY5	06dhy5 homo sapien
431	73	8.0	622	2	Q9V313	Q9v313 dtrosophila	504	71.5	7.9	556	2	0836P9	0836p9 enterococu
432	73	8.0	659	1	UVR8_CLOPE	Q64322 clostridium	505	71.5	7.9	559	2	09DID9	09did9 influenza a
433	73	8.0	742	2	095JY6	095jy6 macaca fasc	506	71.5	7.9	603	2	09Y8U6	09y8u6 aeryopryum p
434	73	8.0	855	2	08CDK1	08cdk1 mus musculu	507	71.5	7.9	617	2	P73606	P73606 synecchocyst
435	73	8.0	947	1	RG43_SOJBU	07x4d0 solanum bul	508	71.5	7.9	632	2	066JY2	066jy2 mus musculu
436	73	8.0	1085	1	CUTT7_SCHRO	P44339 echinosacch	509	71.5	7.9	661	1	UVR8_BACSU	P37934 bacillus su
437	73	8.0	1972	1	MYH8_MOUSE	008638 mus musculu	510	71.5	7.9	731	2	06Z554	06z554 oryza sativ
438	73	8.0	1972	2	08R384	08r384 mus musculu	511	71.5	7.9	820	1	YNH4_CAEBL	P32742 caenorhadi
439	73	8.0	1984	2	0692X3	0692x3 mus musculu	512	71.5	7.9	830	1	GYRA_CLOAB	P94605 clostridium
440	72.5	8.0	166	1	RUVX_RHILLO	098m90 rhizobium 1	513	71.5	7.9	856	2	062121	062121 mus musculu
441	72.5	8.0	208	2	0749B2	0749b2 geobacter s	514	71.5	7.9	887	1	UFO_HUMAN	P30530 homo sapien
442	72.5	8.0	212	2	Q8ND50	Q8nd50 homo sapien	515	71.5	7.9	948	2	08A3E9	08a3e9 bacteroides
443	72.5	8.0	324	2	Q7R3C9	Q7r3c9 giardia lam	516	71.5	7.9	1052	2	07Z7R0	07z7r0 homo sapien
444	72.5	8.0	368	2	06BGA0	06bgao paramecium	517	71.5	7.9	1204	2	094HV3	094hv3 oryza sativ
445	72.5	8.0	374	2	Q7MB01	Q7mb01 photorhabdu	518	71.5	7.9	1204	2	07XRF26	07xrf26 oryza sativ
446	72.5	8.0	456	2	06BHQ4	06bhq4 debaryomyce	519	71.5	7.9	1290	1	RA50_SCHPO	09ut18 schizosacch
447	72.5	8.0	556	2	Q7RI98	Q7ri98 plasmodium	520	71.5	7.9	1489	2	06B145	06b145 debaryomyce
448	72.5	8.0	558	2	Q7MB08	Q7mbg8 vibrio vuln	521	71.5	7.9	1501	2	06B146	06b146 debaryomyce
449	72.5	8.0	568	2	08D4X9	08d4x9 vibrio vuln	522	71.5	7.9	1972	1	MYH8_HUMAN	P35749 homo sapien
450	72.5	8.0	661	2	0659H3	0659h3 bacillus am	523	71.5	7.9	1972	2	096542	096542 dtrosophila
451	72.5	8.0	720	1	08N7X3	08n7x3 homo sapien	524	71.5	7.9	2023	2	09V5Z9	09v5z9 dtrosophila
452	72.5	8.0	721	1	BBS2_HUMAN	09bxc9 homo sapien	525	71.5	7.9	2035	1	NIN_MOUSE	0610k3 mus musculu
453	72.5	8.0	735	2	Q7VSE4	Q7vse4 dtrosophila	526	71.5	7.9	2113	2	0674R4	0674r4 mus musculu
454	72.5	8.0	822	1	WJCE_YEAST	P47061 seccaromyce	527	71.5	7.9	2136	2	09S197	09s197 arabidopsis
455	72.5	8.0	892	1	SYA_HELHP	Q7VHV4 helicobacte	528	71.5	7.9	3200	2	07XEP97	07xep97 oryza sativ
456	72.5	8.0	980	2	024780	024780 clostridium	529	71.5	7.9	5633	2	081454	081454 plasmodium
457	72.5	8.0	1053	2	06BG20	06bg20 paramecium	530	71	7.8	226	1	DP1A_ECOLI	054149 escherichia
458	72.5	8.0	1289	2	068DM1	068dm1 homo sapien	531	71	7.8	288	1	PSTB_MYCPE	088u11 mycoplasma
459	72.5	8.0	1585	2	07Z745	07z745 homo sapien	532	71	7.8	310	2	028810	028810 porcous tr
460	72.5	8.0	2241	2	08IKJ7	08ikj7 plasmodium	533	71	7.8	316	2	073516	073516 bacillus ce
461	72.5	8.0	2411	2	06CXV6	06cxv6 kluyveromyc	534	71	7.8	316	2	081BM4	081bm4 bacillus ce
462	72.5	8.0	3911	1	AKA9_HUMAN	099996 h a-kinase	535	71	7.8	353	2	09JMP1	09j1m1 bacteriophe
463	72	7.9	127	2	08B598	08b598 asinine her	536	71	7.8	372	2	09PJF1	09pd46 neuropept
464	72	7.9	247	2	07VY22	064848 porcine ade	537	71	7.8	389	2	MAT1_COCSA	09pd46 neuropept
465	72	7.9	297	2	07VY22	07vy22 cryptospori	538	71	7.8	415	2	09LNR6	09lea30 neuropept
466	72	7.9	319	2	06SFT9	06sft9 uncultured	539	71	7.8	445	2	09LNR6	09lea30 neuropept
467	72	7.9	341	2	06D077	06d077 erwina car	540	71	7.8	474	2	096W63	096w63 arabidopsis
468	72	7.9	341	2	06R1L1	06r1l1 cricetus	541	71	7.8	503	1	CPV1_LAGAC	096f66 lagenorhync
469	72	7.9	381	2	08FSM7	08fsm7 corynebacte	542	71	7.8	505	1	RADA_SYNY3	P743391 synecchocyst

543	71	7.8	552	2	Q6NSCO	Q6NSCO	homo sapien	616	70	7.7	431	2	Q8SXY7	Q8SXY7	drosophila
544	71	7.8	634	2	Q8P3C2	Q8P3C2	xanthomonas	617	70	7.7	438	2	Q9MVZ4	Q9MVZ4	leucodon at
545	71	7.8	641	2	Q7RXA7	Q7RXA7	neutrospora	618	70	7.7	448	1	RUI7_DROME	RUI7_DROME	drosophila
546	71	7.8	713	2	Q7NSZ9	Q7NSZ9	photobabu	619	70	7.7	448	2	Q974Y6	Q974Y6	sulfolobus
547	71	7.8	716	1	HOK2_MOUSE	Q7mk6	mus musculus	620	70	7.7	449	2	Q9CS90	Q9CS90	arabidopsis
548	71	7.8	716	2	HOK2_MOUSE	Q66Jv2	mus musculus	621	70	7.7	463	2	Q8PP23	Q8PP23	xanthomonas
549	71	7.8	722	2	Q8YRW1	Q8YRW1	mus musculus	622	70	7.7	493	2	P957J2	P957J2	salmonella
550	71	7.8	757	1	PEPX_STRPN	Q9Jrc8	streptococc	623	70	7.7	508	2	Q6NVR6	Q6NVR6	xenopus tro
551	71	7.8	757	1	PEPX_STRK6	Q8qk87	streptococc	624	70	7.7	513	2	Q9LRU0	Q9LRU0	tritium ae
552	71	7.8	806	1	NH48_CAEEL	Q94407	caenorhabdi	625	70	7.7	541	2	Q7S5S5	Q7S5S5	neutrospora
553	71	7.8	880	1	SYL_HELPJ	Q9Jf63	helicobacte	626	70	7.7	573	2	Q6ELP0	Q6ELP0	caenorhabdi
554	71	7.8	857	2	Q7PDH6	Q9Jdh6	anopheles g	627	70	7.7	584	2	Q97H15	Q97H15	clostridium
555	71	7.8	1029	2	Q63BK4	Q63bk4	bacillus ce	628	70	7.7	587	2	Q9RA89	Q9RA89	sinorhizobi
556	71	7.8	1029	2	Q81Q09	Q81qg9	bacillus an	629	70	7.7	600	2	Q15516	Q15516	homo sapien
557	71	7.8	1029	2	Q6HJ13	Q6hj13	bacillus th	630	70	7.7	663	2	Q756H5	Q756H5	ashbya goss
558	71	7.8	1271	2	Q8A321	Q8a321	bacteroides	631	70	7.7	675	2	Q82J52	Q82J52	streptomyce
559	71	7.8	1472	2	Q81U0U	Q81u0u	plasmodium	632	70	7.7	686	2	Q71RW7	Q71RW7	pantoea agg
560	71	7.8	1749	2	Q81IM5	Q81im5	plasmodium	633	70	7.7	714	2	Q15718	Q15718	dictyosteli
561	71	7.8	1761	2	Q81091	Q81091	plasmodium	634	70	7.7	742	2	Q7X4V0	Q7X4V0	bacillus ce
562	71	7.8	2819	2	Q98QF8	Q98qf8	mycoplasma	635	70	7.7	742	2	Q7X4V1	Q7X4V1	bacillus an
563	70.5	7.8	153	2	Q8C8P3	Q8c8p3	m mus muscu	636	70	7.7	792	2	Q9BP03	Q9BP03	dictyosteli
564	70.5	7.8	185	2	Q800H0	Q800h0	brachydanio	637	70	7.7	795	2	Q751F8	Q751F8	ashbya goss
565	70.5	7.8	196	2	Q76KAS	Q76kas	brachydanio	638	70	7.7	823	2	Q73FK0	Q73FK0	bacillus ce
566	70.5	7.8	231	2	Q6CPN5	Q6cpn5	kluyveromyc	639	70	7.7	823	2	Q81W30	Q81W30	bacillus an
567	70.5	7.8	248	1	P90930	P90930	caenorhabdi	640	70	7.7	823	2	Q6H009	Q6H009	bacillus th
568	70.5	7.8	253	1	P8TB_CLOPE	Q8mp8	clostridium	641	70	7.7	890	2	Q45S87	Q45S87	caenorhabdi
569	70.5	7.8	265	2	Q639N3	Q639n3	bacillus ce	642	70	7.7	939	2	Q7Q3F0	Q7Q3F0	anopheles g
570	70.5	7.8	265	2	Q923V9	Q923v9	pseudomonas	643	70	7.7	1067	1	SVI_PYRAB	SVI_PYRAB	pyrococcus
571	70.5	7.8	316	1	GSBH_PHOLL	Q7m7h8	photobabu	644	70	7.7	1157	2	Q6NPI4	Q6NPI4	drosophila
572	70.5	7.8	349	2	Q7VIT4	Q7vit4	helicobacte	645	70	7.7	1310	2	Q86IX0	Q86IX0	dictyosteli
573	70.5	7.8	357	2	Q95J20	Q95j20	homo sapien	646	70	7.7	2871	1	DESP_HUMAN	DESP_HUMAN	homo sapien
574	70.5	7.8	381	2	Q6D855	Q6d855	erwinia car	647	70	7.7	3218	2	Q9W3V6	Q9W3V6	drosophila
575	70.5	7.8	415	2	Q9SJW7	Q9sjw7	arabidopsis	648	70	7.7	120	2	Q9NHW1	Q9NHW1	plasmodium
576	70.5	7.8	425	2	Q6AYE4	Q6aye4	rattus norv	649	70	7.7	224	2	Q678L1	Q678L1	mus musculus
577	70.5	7.8	513	2	Q6CR31	Q6cr31	kluyveromyc	650	70	7.7	285	2	Q9L3N0	Q9L3N0	microcycis
578	70.5	7.8	519	1	Y964_STARP	Q8sc67	staphylococ	651	70	7.7	415	2	Q50861	Q50861	mycobacteri
579	70.5	7.8	550	2	Q8N7M4	Q8n7m4	homo sapien	652	70	7.7	415	2	Q70J57	Q70J57	microcycis
580	70.5	7.8	558	2	Q9X225	Q9x225	thermotoga	653	70	7.7	417	2	Q6D4N9	Q6D4N9	erwinia car
581	70.5	7.8	656	1	YC26_PORPU	P51392	porphyra pu	654	70	7.7	427	2	Q99160	Q99160	mus musculus
582	70.5	7.8	660	1	LYRB_BACHD	Q9kx69	bacillus ha	655	70	7.7	437	2	Q6P8A4	Q6P8A4	mus musculus
583	70.5	7.8	713	1	HOK2_HUMAN	Q9ged9	homo sapien	656	70	7.7	452	2	P73256	P73256	synechocyst
584	70.5	7.8	739	2	Q66JH2	Q9Jf62	mus musculus	657	70	7.7	457	1	BAG4_HUMAN	BAG4_HUMAN	homo sapien
585	70.5	7.8	839	2	Q97FP4	Q97fp4	clostridium	658	70	7.7	476	2	Q647Q8	Q647Q8	uncultured
586	70.5	7.8	863	1	M5P_ECHGR	P35417	echinococcu	659	70	7.7	505	2	Q6B129	Q6B129	debaromyce
587	70.5	7.8	863	1	M5P_TAESA	Q81305	taenia sagi	660	70	7.7	526	2	Q8K4T6	Q8K4T6	rattus norv
588	70.5	7.8	863	1	M5P_TAESO	P35418	taenia sagi	661	70	7.7	541	2	Q941J3	Q941J3	zea mays (m
589	70.5	7.8	863	2	Q68JF3	Q68j63	taenia soli	662	70	7.7	572	2	Q61FZ6	Q61FZ6	mus musculus
590	70.5	7.8	892	1	RA16_SCHPO	P36617	schizosacch	663	70	7.7	594	2	Q73927	Q73927	squarus aca
591	70.5	7.8	1029	2	P91176	P91176	caenorhabdi	664	70	7.7	610	2	Q66FY3	Q66FY3	yersinia pe
592	70.5	7.8	1039	2	Q23461	Q23461	arabidopsis	665	70	7.7	610	2	Q8ZAG8	Q8ZAG8	yersinia pe
593	70.5	7.8	1137	2	Q8B159	Q8b159	mus musculus	666	70	7.7	623	2	Q72QY7	Q72QY7	leptospi
594	70.5	7.8	1192	2	Q8B179	Q8b179	mus musculus	667	70	7.7	623	2	Q8F4V3	Q8F4V3	leptospi
595	70.5	7.8	1235	2	Q8SX64	Q8sx64	drosophila	668	70	7.7	625	2	Q6IMF3	Q6IMF3	rattus norv
596	70.5	7.8	1254	2	Q81ZW9	Q81zw9	homo sapien	669	70	7.7	661	2	Q65ED8	Q65ED8	bacillus li
597	70.5	7.8	1264	2	Q8GUS6	Q8gus6	oryza sativ	670	70	7.7	662	2	Q80MS5	Q80MS5	mus musculus
598	70.5	7.8	1296	2	Q86UW7	Q86uw7	homo sapien	671	70	7.7	669	2	Q8BT4	Q8BT4	m mus muscu
599	70.5	7.8	1328	2	Q6FT10	Q6ft10	candida gla	672	70	7.7	675	2	Q8BMT4	Q8BMT4	m mus muscu
600	70.5	7.8	1381	2	Q9VZT7	Q9vzt7	drosophila	673	70	7.7	721	2	Q8BU17	Q8BU17	mus musculus
601	70.5	7.8	1450	2	Q8S119	Q8s119	oryza sativ	674	70	7.7	746	2	Q7VPE6	Q7VPE6	haemophilus
602	70.5	7.8	1515	2	Q6AVS6	Q6avs6	oryza sativ	675	70	7.7	788	2	Q8SVG1	Q8SVG1	drosophila
603	70.5	7.8	1759	2	Q72PFO	Q72pf0	leptospi	676	70	7.7	822	2	Q9W4N2	Q9W4N2	yersinia pe
604	70.5	7.8	1759	2	Q8F6Y5	Q8f6y5	leptospi	677	70	7.7	822	2	Q66B31	Q66B31	yersinia ps
605	70.5	7.8	2270	2	Q813B5	Q813b5	plasmodium	678	70	7.7	832	2	Q6FNV5	Q6FNV5	yersinia pe
606	70.5	7.8	179	2	Q9KBA2	Q9kba2	bacillus ha	679	70	7.7	843	2	Q6FNV5	Q6FNV5	candida gla
607	70.5	7.8	209	2	Q8A8G4	Q8a8g4	bacteroides	680	70	7.7	843	2	Q74UL6	Q74UL6	yersinia pe
608	70.5	7.7	241	2	Q7MOS9	Q7mg9	wolfinella s	681	70	7.7	860	2	Q9F8N0	Q9F8N0	arabidopsis
609	70.5	7.7	316	2	Q639G4	Q639g4	bacillus ce	682	70	7.7	866	2	Q25517	Q25517	helicobacte
610	70.5	7.7	326	2	Q7NMU0	Q7njd0	gloeobacter	683	70	7.7	894	2	Q8N5L2	Q8N5L2	homo sapien
611	70.5	7.7	332	2	Q6HMO1	Q6hmq1	bacillus th	684	70	7.7	912	2	Q6CEZ7	Q6CEZ7	dictyosteli
612	70.5	7.7	332	2	Q8YND8	Q8ynd8	anabaena sp	685	70	7.7	1041	2	Q7KWK7	Q7KWK7	dictyosteli
613	70.5	7.7	357	2	Q63168	Q63168	burkholderi	686	70	7.7	1139	1	LIPA_CAEEL	LIPA_CAEEL	caenorhabdi
614	70.5	7.7	385	2	Q64V44	Q64v44	bacteroides	687	70	7.7	1139	1	Q8X059	Q8X059	neutrospora
615	70.5	7.7	399	2	Q9V2E1	Q9v2e1	pyrococcus	688	70	7.7	1313	2			

689	69.5	7.7	1508	2	06BVU5	06bvus debaryomyce	762	68.5	7.6	207	2	06SGZ5	06sgz5 uncultured
690	69.5	7.7	1707	2	08YU2	08yuz arabana sp	763	68.5	7.6	207	2	06UC9	06uc9 uncultured
691	69.5	7.7	2052	2	07XW5	07xw5 oryza sativ	764	68.5	7.6	208	2	07ZCF5	07zcf5 desulfovibr
692	69.5	7.7	2223	2	08ID12	08id12 plasmodium	765	68.5	7.6	208	1	RS4_THENA	09x13 thermotoga
693	69	7.6	114	2	09MCW2	09mcw2 bacterioph	766	68.5	7.6	220	2	06UK17	06uk17 capsicum an
694	69	7.6	116	2	064HN7	064hn7 bacterioph	767	68.5	7.6	240	2	065GA9	065ga9 bacillus ii
695	69	7.6	164	2	053357	053357 lactococcus	768	68.5	7.6	252	2	09BLO5	09bl05 leishmania
696	69	7.6	205	2	083VA7	083va7 western x p	769	68.5	7.6	294	2	06AVJ9	06avj9 desulfotale
697	69	7.6	206	1	RS4_BUCAP	P41166 buchiera ap	770	68.5	7.6	295	2	08XNT6	08xnt6 streptylcoc
698	69	7.6	220	1	KAD_PYRFU	08u207 pyrococcus	771	68.5	7.6	295	2	06GBH9	06gbh9 streptylcoc
699	69	7.6	231	2	Q7Q681	Q7q681 anopheles g	772	68.5	7.6	301	2	08ITG8	08itg8 methanosaer
700	69	7.6	247	2	063GQ6	Q63gq6 bacillus ce	773	68.5	7.6	304	2	07RCL1	07rcl1 plasmodium
701	69	7.6	265	2	Q7QMP3	Q7mq3 vibrio vuln	774	68.5	7.6	332	2	07RCL4	07rcl4 plasmodium
702	69	7.6	265	2	08DDA9	08dda9 vibrio vuln	775	68.5	7.6	332	2	09GZS5	09gzs5 sulfolobus
703	69	7.6	272	1	HAT5_AKATH	002283 arabidopsis	776	68.5	7.6	363	2	06VXP5	06vxp5 onion yello
704	69	7.6	290	2	06N757	06n757 rhodospheudo	777	68.5	7.6	364	2	083SD5	083sd5 shigella fl
705	69	7.6	312	2	0823T9	0823t9 chlamydomph	778	68.5	7.6	367	1	MTCL_CHV13	P36216 chlorella v
706	69	7.6	321	2	06D2B4	06d2b4 erwinia car	779	68.5	7.6	392	1	RRP_SVS	P11208 simian viru
707	69	7.6	346	1	LYSK_SUNSO	Q580W5 sulfolobus	780	68.5	7.6	392	2	06H8K8	06h8k8 simian para
708	69	7.6	349	1	TAFF_HUMAN	Q15545 homo sapien	781	68.5	7.6	398	2	07OIA8	07oia8 anopheles g
709	69	7.6	365	2	08DRV3	08drv3 streptococc	782	68.5	7.6	414	2	08R6T9	08r6t9 thermocaneer
710	69	7.6	415	2	06ETC9	06etc9 oryza sativ	783	68.5	7.6	417	2	06VT00	06vt00 vibrio para
711	69	7.6	421	1	RFL_METUA	Q58239 methanococc	784	68.5	7.6	431	1	SGK1_HUMAN	000141 homo sapien
712	69	7.6	438	2	Q9MVX2	Q9mvx2 myiabea fru	785	68.5	7.6	431	1	SGK1_MOUSE	Q9wv66 mus musculu
713	69	7.6	482	1	K2C8_HUMAN	P05787 homo sapien	786	68.5	7.6	431	2	068G05	068g05 ratius norv
714	69	7.6	482	1	K2C8_RAT	Q10758 ratius norv	787	68.5	7.6	442	1	TRME_MYCPN	P5104 mycoplasma
715	69	7.6	483	2	06GNT0	06gnt0 homo sapien	788	68.5	7.6	456	2	08KA3	08ka3 streptococc
716	69	7.6	486	2	080WH8	080wh8 rattus sp.	789	68.5	7.6	468	2	08IR66	08ir66 bacillus an
717	69	7.6	486	2	Q91WT0	Q91wt0 mus musculu	790	68.5	7.6	481	2	07XNT0	07xnt0 oryza sativ
718	69	7.6	496	2	08ENB3	Q8enb3 oceanobacil	791	68.5	7.6	487	2	023501	Q23501 arabidopsis
719	69	7.6	501	2	0659X5	0659x5 escherichia	792	68.5	7.6	494	2	07TH54	07th54 influenza a
720	69	7.6	504	2	08PSS5	08pss5 corynebacte	793	68.5	7.6	497	2	085YR0	085yr0 euphorbia s
721	69	7.6	505	2	06P4C7	06p4c7 homo sapien	794	68.5	7.6	502	2	08MTC9	08mtc9 helicobis z
722	69	7.6	505	2	08RV51	08rv51 oryza sativ	795	68.5	7.6	504	1	SIX1_YEAST	012460 saccharomyc
723	69	7.6	505	2	Q7X716	Q7x716 oryza sativ	796	68.5	7.6	519	2	06NS85	Q6ns85 mus musculu
724	69	7.6	509	2	Q9LRT9	Q9lrt9 triticum ae	797	68.5	7.6	539	2	08K4V4	08k4v4 ratius norv
725	69	7.6	513	1	RMUC_VIBCH	Q94g13 physcomltre	798	68.5	7.6	546	2	06VZN1	06vzn1 oryza sativ
726	69	7.6	533	2	Q94G13	Q94g13 physcomltre	799	68.5	7.6	552	2	08DVB0	08dvb0 streptococc
727	69	7.6	567	2	08H0N7	08h0n7 populus tri	800	68.5	7.6	583	2	074WJ2	074wj2 versinia pe
728	69	7.6	576	2	0659H4	0659h4 bacillus am	801	68.5	7.6	590	2	066CF2	066cf2 versinia ps
729	69	7.6	582	2	06W915	06w915 paramectium	802	68.5	7.6	590	2	08ZG79	08zg79 versinia pe
730	69	7.6	613	2	06PG44	06pg44 homo sapien	803	68.5	7.6	621	2	06BE26	06be26 citrus unsh
731	69	7.6	633	2	06B8K3	06b8k3 gracillaria	804	68.5	7.6	694	2	Q91870	Q91870 xenopus lae
732	69	7.6	633	2	UVRB_PSEAE	P21174 pseudomonas	805	68.5	7.6	694	2	Q7ZYN2	Q7zyn2 xenopus lae
733	69	7.6	691	2	Q756Y5	Q756y5 abhya goss	806	68.5	7.6	718	2	08SMD8	08smd8 cephalicito
734	69	7.6	715	2	P73259	P73259 streptococyt	807	68.5	7.6	741	1	PI03_MOUSE	Q9j0e1 mus musculu
735	69	7.6	724	1	HMMR_HUMAN	Q75330 homo sapien	808	68.5	7.6	741	2	0811A5	0811a5 ratius norv
736	69	7.6	732	2	08CGT0	08cgt0 mus musculu	809	68.5	7.6	768	2	06LJR3	06ljr3 solanum dem
737	69	7.6	799	2	08MT65	Q8mt65 eupletes oc	810	68.5	7.6	803	2	06FLS7	06fls7 candida gla
738	69	7.6	809	2	Q7PT27	Q7pt27 anopheles g	811	68.5	7.6	803	2	Q9P382	Q9p382 schizosacch
739	69	7.6	833	2	Q96442	Q96442 strongyloce	812	68.5	7.6	836	1	NOT3_YEAST	P6102 saccharomyc
740	69	7.6	860	2	Q93091	Q93091 human immun	813	68.5	7.6	836	2	06B2J3	06b2j3 saccharomyc
741	69	7.6	871	2	Q7TWT0	Q7twt0 mus musculu	814	68.5	7.6	843	1	VAV_RAT	P54100 ratius norv
742	69	7.6	879	2	Q76978	Q76978 scypha raph	815	68.5	7.6	875	2	Q9ZK28	Q9zkr8 helicobacte
743	69	7.6	893	2	Q6DC15	Q6dc15 xenopus lae	816	68.5	7.6	879	2	08V199	08v199 ratius norv
744	69	7.6	978	2	066HN7	Q66hn7 dictyoscelei	817	68.5	7.6	888	2	06PE80	06pe80 mus musculu
745	69	7.6	986	1	PPOL_SARPE	Q11208 sarcoptero	818	68.5	7.6	888	2	08VY03	08vy03 ratius norv
746	69	7.6	1081	2	09GNT2	Q9gnt2 paracentroc	819	68.5	7.6	888	2	08VOY0	08voy0 mus musculu
747	69	7.6	1081	2	09GOS8	Q9gos8 strongyloce	820	68.5	7.6	920	2	Q9E176	Q9e176 rhodococcus
748	69	7.6	1153	2	Q92UC1	Q92uc1 rickettsia	821	68.5	7.6	935	1	IF38_MEDTR	Q9xhnl medicago tr
749	69	7.6	1182	2	08CBA7	Q8cba7 mus musculu	822	68.5	7.6	937	2	Q9XGF5	Q9xgfs solanum tub
750	69	7.6	1237	1	KEB1_RABIT	P18688 oryctolagus	823	68.5	7.6	938	2	Q9SM52	Q9sm52 solanum aca
751	69	7.6	1349	2	Q6RCM0	Q6rcm0 entamoeba h	824	68.5	7.6	948	2	Q9KPD4	Q9kpd4 vibrio chol
752	69	7.6	1437	2	08VDC1	Q8vdc1 mus musculu	825	68.5	7.6	988	2	Q7XIH2	Q7xih2 oryza sativ
753	69	7.6	1486	2	06LPL5	Q6lpl5 photobacter	826	68.5	7.6	1039	1	SYI_METUA	Q58333 methanococc
754	69	7.6	1633	2	088QC4	Q88qc4 pseudomonas	827	68.5	7.6	1108	2	063J03	Q63j03 bacillus ce
755	69	7.6	1860	2	06AVU8	Q6avu8 oryza sativ	828	68.5	7.6	1108	2	081KY5	081ky5 bacillus an
756	69	7.6	1898	2	06FNX9	Q6fnx9 candida gla	829	68.5	7.6	1108	2	06HCS8	Q6hcs8 bacillus th
757	69	7.6	1972	1	MYHB_RABIT	P35748 oryctolagus	830	68.5	7.6	1114	2	Q9NE53	Q9nes3 leishmania
758	69	7.6	2426	2	Q7PLZ8	Q7plz8 anopheles g	831	68.5	7.6	1132	1	DNBI_HHV6U	P52338 human herpe
759	68.5	7.6	153	2	Q9KRA3	Q9kra3 vibrio chol	832	68.5	7.6	1132	1	DNBI_HHV6Z	P52538 human herpe
760	68.5	7.6	206	2	RS4_CLOTE	Q930q9 clostridium	833	68.5	7.6	1132	2	Q785N4	Q785n4 human herpe
761	68.5	7.6	207	1	RS4_CANBP	Q7vqc4 candidatus	834	68.5	7.6	1162	1	SA2_MOUSE	Q15638 mus musculu

835	68.5	7.6	1162	2	06NZN7	06NZN7 mus musculus	908	68	7.5	622	2	014794	014794 homo sapien
836	68.5	7.6	1242	1	KPB1_RAT	06649 rattus norv	909	68	7.5	625	2	07NBZ6	07NBZ6 mycoplasma
837	68.5	7.6	1270	2	06DKA2	066k2 xenopus lae	910	68	7.5	639	2	0883E2	0883E2 pseudomonas
838	68.5	7.6	1292	2	06CF42	06cf42 yarrowia li	911	68	7.5	641	2	075CX7	075CX7 ashbya gos
839	68.5	7.6	1410	2	06NNX2	06nnx2 drosophila	912	68	7.5	696	2	08XQ93	08XQ93 ralsstonia s
840	68.5	7.6	1641	2	09VQ76	09vq76 drosophila	913	68	7.5	764	2	08LIL8	08LIL8 oryza sativ
841	68.5	7.6	1960	2	08S6N2	08s6n2 oryza sativ	914	68	7.5	809	1	SYL_CAMJB	09pnk3 campylobact
842	68.5	7.6	2291	2	SPCB_DROME	000963 drosophila	915	68	7.5	842	1	CULB_YEAST	07050 saccharomyc
843	68.5	7.6	2818	2	Q7SE15	Q7se15 neurospora	916	68	7.5	851	1	Q75OF1	Q75OF1 ashbya gos
844	68	7.5	118	2	Q64HNS	064hns bacterioph	917	68	7.5	902	2	06BZAI	06BZAI debaryomyce
845	68	7.5	244	2	Q9V0X5	09v0x5 pyrococcus	918	68	7.5	990	1	SUI2_DROME	08jz9 drosophila
846	68	7.5	247	1	PCPC_SPHCR	003520 sphinobium	919	68	7.5	908	2	0871E8	0871E2 vibrio algi
847	68	7.5	257	2	08FO19	08fo19 corynebacte	920	68	7.5	973	2	074698	074698 candida alb
848	68	7.5	259	2	Q7UKJ7	Q7ukj7 rhodospirill	921	68	7.5	981	2	080UK9	080UK9 mus musculu
849	68	7.5	263	2	Q76Z89	Q76z89 helicoidari	922	68	7.5	994	1	MERK_MOUSE	060805 mus musculu
850	68	7.5	283	2	Q7MG66	Q7mg66 vibrio vuln	923	68	7.5	1004	2	08UMH4	08umh4 human immun
851	68	7.5	297	2	06LJ73	06lj73 photobacter	924	68	7.5	1038	2	08VCU3	08vcu3 mus musculu
852	68	7.5	300	2	Q9XZS8	09xz88 escherichia	925	68	7.5	1038	2	08CC88	08cc88 mus musculu
853	68	7.5	316	1	PGLB_CHICK	090944 gallus gall	926	68	7.5	1046	2	08J1Z6	08j1z6 iridovirus
854	68	7.5	326	1	SYRM_RHIME	P18561 rhizobium m	927	68	7.5	1063	2	093959	093959 candida alb
855	68	7.5	338	2	08UKC5	08ukc5 agrobacteri	928	68	7.5	1162	1	SA2_HUMAN	09h3u4 homo sapien
856	68	7.5	347	1	SH33_HUMAN	099963 homo sapien	929	68	7.5	1183	2	Q7T005	Q7T005 brachydanio
857	68	7.5	347	2	Q93RQ6	Q93rq6 streptococc	930	68	7.5	1231	2	06A102	06a102 homo sapien
858	68	7.5	361	2	Q7D3N9	Q7d3n9 agrobacteri	931	68	7.5	1231	2	06MZM4	06mzm4 homo sapien
859	68	7.5	365	2	08XJ35	08xj35 clostridium	932	68	7.5	1231	2	06MZM4	06mzm4 homo sapien
860	68	7.5	371	1	TCT_PSESM	0887b0 pseudomonas	933	68	7.5	1268	2	068DE9	068de9 homo sapien
861	68	7.5	380	1	BIOP_HAETIN	P44422 haemophilus	934	68	7.5	1318	2	Q7QAJ3	Q7qaj3 anopheles g
862	68	7.5	391	2	08K5V9	08k5v9 streptococc	935	68	7.5	1333	2	086K99	086k99 dictyostell
863	68	7.5	411	2	08CES2	08ces2 mus musculu	936	68	7.5	1355	2	06FXJ5	06fxj5 candida gla
864	68	7.5	434	2	Q6M3S7	06m3s7 brachythecl	937	68	7.5	1680	2	09P1Z9	09p1z9 homo sapien
865	68	7.5	440	1	SCRC_HUMAN	P47872 homo sapien	938	68	7.5	1708	2	068DP5	068dp5 homo sapien
866	68	7.5	440	2	Q8IV17	Q8iv17 homo sapien	939	68	7.5	2139	2	007569	007569 entamoeba h
867	68	7.5	441	2	Q9MVX1	Q9mvx1 tulidum re	940	68	7.5	2240	1	CD89_DROME	Q9veu1 drosophila
868	68	7.5	444	1	RBL_BOTST	P36477 botrytis ma	941	68	7.5	2357	2	Q9DGM6	Q9dgm6 brachydanio
869	68	7.5	450	2	Q79MP4	Q79mp4 aspergilla m	942	68	7.5	4524	2	0813J9	0813j9 plasmodium
870	68	7.5	465	2	Q9GIF7	Q9gif7 brochelella	943	68	7.5	5255	1	BACA_BACLI	088006 b bacteri
871	68	7.5	471	2	Q9FP75	Q9fp75 arabidopsis	944	68	7.5	5317	2	08TA74	08ta74 hemientroc
872	68	7.5	473	2	Q8DUJ7	Q8duj7 synechococc	945	67.5	7.4	109	2	Q9V0Z2	Q9v0z2 pyrococcus
873	68	7.5	475	2	08HM59	08hm59 trimegialacti	946	67.5	7.4	135	2	P914I7	P914i7 caenorhabdi
874	68	7.5	475	2	Q95G49	Q95g49 trimegialacti	947	67.5	7.4	145	2	08JRV8	08jrv8 plithorimaea
875	68	7.5	475	2	Q9GIF8	Q9gif8 brochelella	948	67.5	7.4	170	2	064RJ5	064rj5 bacteroides
876	68	7.5	475	2	Q9TM67	Q9tm67 heterophyll	949	67.5	7.4	211	2	06YQJ6	06yqj6 onion yello
877	68	7.5	475	2	Q9TM65	Q9tm65 wijkia horn	950	67.5	7.4	215	2	086EV1	086ev1 schistosoma
878	68	7.5	475	2	Q9TM66	Q9tm66 brochelella	951	67.5	7.4	251	2	P891J3	P891j3 sida golden
879	68	7.5	475	2	Q9TM73	Q9tm73 boulaya mit	952	67.5	7.4	253	2	Q8WID7	Q8wid7 acridocarpu
880	68	7.5	489	2	Q09051	Q09051 escherichia	953	67.5	7.4	254	2	Q8WLD7	Q8wld7 homo sapien
881	68	7.5	490	2	Q9DBH4	Q9dbh4 mus musculu	954	67.5	7.4	267	2	08NDK7	Q8ndk7 tricomaria
882	68	7.5	493	2	08XB70	08xb70 escherichia	955	67.5	7.4	300	2	Q9SLI6	Q9slj6 arabidopsis
883	68	7.5	500	2	Q6FP06	06fp06 candida gla	956	67.5	7.4	302	2	06LPU3	06lpj3 photobacter
884	68	7.5	501	2	Q820Z7	Q820z7 shigella fl	957	67.5	7.4	319	2	Q8DHP4	Q8dhp4 synechococc
885	68	7.5	503	1	CPV1_CAPHI	06y121 capra hircu	958	67.5	7.4	326	2	Q71V08	Q71v08 homo sapien
886	68	7.5	503	1	CPV1_SHEEP	Q9x828 ovis aries	959	67.5	7.4	328	2	Q7W6Z8	Q7w6z8 bordetella
887	68	7.5	507	2	Q9SM61	Q9sm61 callithrix	960	67.5	7.4	360	2	Q659W3	Q659w3 homo sapien
888	68	7.5	507	2	Q8FA66	Q8fa66 escherichia	961	67.5	7.4	372	2	Q7Z3H1	Q7z3h1 homo sapien
889	68	7.5	511	2	Q90Z87	Q90z87 kana cateab	962	67.5	7.4	373	2	Q8FUF3	Q8fuf3 corynebacte
890	68	7.5	514	2	Q94IP9	Q94ip9 lycopersico	963	67.5	7.4	381	2	Q6A6I1	Q6a6i1 propionibac
891	68	7.5	537	2	Q93IEP9	Q93iep9 photorhabdu	964	67.5	7.4	384	1	A1PL_HUMAN	Q9gnz3 homo sapien
892	68	7.5	545	2	Q7QX89	Q7qx89 giardia lam	965	67.5	7.4	384	1	A1PL_PANPA	Q9smn3 pan panlicu
893	68	7.5	557	2	Q8A9T0	Q8a9t0 bacteroides	966	67.5	7.4	387	2	Q6CLZ4	Q6clz4 kluyveromyc
894	68	7.5	562	2	Q91V02	Q91v02 human immun	967	67.5	7.4	396	2	Q8BZY9	Q8bzy9 mus musculu
895	68	7.5	564	2	Q74Z82	Q74z82 ashbya gos	968	67.5	7.4	412	2	Q8SVZ5	Q8svz5 mus musculu
896	68	7.5	567	2	Q6JSH3	Q6jsh3 haemophilus	969	67.5	7.4	423	2	Q8ND86	Q8nd86 homo sapien
897	68	7.5	573	2	Q6E1P3	Q6eip3 bacillus th	970	67.5	7.4	425	2	Q6FPQ5	Q6fpq5 candida gla
898	68	7.5	573	2	Q6E1R9	Q6e1r9 bacillus sp	971	67.5	7.4	427	2	Q8SVP6	Q8svp6 encephalito
899	68	7.5	573	2	Q6E1S1	Q6e1s1 bacillus sp	972	67.5	7.4	428	2	Q72LS2	Q72ls2 leptospira
900	68	7.5	573	2	Q6E1S2	Q6e1s2 geobacillus	973	67.5	7.4	428	2	Q8EY80	Q8ey80 leptospira
901	68	7.5	573	2	Q6E1S3	Q6e1s3 geobacillus	974	67.5	7.4	454	2	Q9SVG1	Q9svg1 arabidopsis
902	68	7.5	573	2	Q6E1S4	Q6e1s4 geobacillus	975	67.5	7.4	457	2	Q9SZM4	Q9szm4 arabidopsis
903	68	7.5	580	2	Q9Z0F2	Q9z0f2 mus musculu	976	67.5	7.4	457	2	Q68A86	Q68a86 paratrichy
904	68	7.5	583	2	Q9Z2U2	Q9z2u2 mus musculu	977	67.5	7.4	511	1	NIFK_SYN8	Q55030 synechococ
905	68	7.5	583	2	Q9Z2C5	Q9z2c5 arabidopsis	978	67.5	7.4	514	2	Q7PR88	Q7pr88 anopheles g
906	68	7.5	588	2	Q14729	Q14729 homo sapien	979	67.5	7.4	515	2	Q9CSW7	Q9csw7 arabidopsis
907	68	7.5	601	2	Q7SXW3	Q7sxw3 brachydanio	980	67.5	7.4	538	2	Q71A12	Q71a12 anaplasma m

981	67.5	7.4	539	2	06NXH9	06xrh9 mus musculus	1054	67	7.4	424	2	08T8M7	08t8m7 caenorhabdi
982	67.5	7.4	553	2	06IG03	06ig03 rictus norv	1055	67	7.4	429	2	094DF7	094df7 oryza sativ
983	67.5	7.4	555	2	09AV96	09av96 nictotiana t	1056	67	7.4	433	2	07ZTM4	07ztm4 brachydanio
984	67.5	7.4	565	2	07OC70	07oc70 anopheles g	1057	67	7.4	435	2	09DWB4	09dwb4 rat cytoomeg
985	67.5	7.4	568	2	08OTC3	08otc3 mus musculu	1058	67	7.4	437	2	03J379	03j379 heilantus
986	67.5	7.4	583	2	08KMJ3	08kmj3 enterococcu	1059	67	7.4	438	2	08HT25	08ht25 isopletygio
987	67.5	7.4	616	2	06LIP9	06lip9 photobacter	1060	67	7.4	439	2	07VIA9	07via9 prochloroco
988	67.5	7.4	635	2	06PQF9	06pqf9 anaplasma c	1061	67	7.4	446	2	0966M4	0966m4 caenorhabdi
989	67.5	7.4	657	2	06DD29	06dd29 xenopus lae	1062	67	7.4	457	2	070BL2	070bl2 mortierella
990	67.5	7.4	680	2	015740	015740 dictyosteli	1063	67	7.4	457	2	09UVV3	09uvv3 mortierella
991	67.5	7.4	719	2	09Y7B1	09y7b1 picchia past	1064	67	7.4	464	2	07V9F3	07v9f3 prochloroco
992	67.5	7.4	721	2	086M11	086m11 drosophila	1065	67	7.4	471	1	RFCL_HALNT1	rfcl_halnt1
993	67.5	7.4	722	2	09XC22	09xc22 mycoplasma	1066	67	7.4	475	1	Q94NB0	q94nb0 gliosadefiph
994	67.5	7.4	723	2	06MSC5	06msc5 mycoplasma	1067	67	7.4	475	2	08SV62	08sv62 cratoneuron
995	67.5	7.4	758	2	06CPJ9	06cpj9 kluyveromyc	1068	67	7.4	475	2	09TMS9	09tms9 myuroclada
996	67.5	7.4	773	2	0806J1	0806j1 arabidopsis	1069	67	7.4	488	1	KIIS_CAMEL	kiis_camel
997	67.5	7.4	801	2	06N0J2	06n0j2 homo sapien	1070	67	7.4	488	2	086LTF	086ltf caenorhabdi
998	67.5	7.4	805	2	06F349	06f349 oryza sativ	1071	67	7.4	492	2	08RSV1	08rsv1 anopheles g
999	67.5	7.4	805	2	07MQJ4	07mqj4 vibrio vuln	1072	67	7.4	495	2	08RSV1	08rsv1 leptotrix
1000	67.5	7.4	805	2	08DDJ2	08ddj2 vibrio vuln	1073	67	7.4	503	1	CPV1_BOVIN	cpv1_bov
1001	67.5	7.4	837	2	06CKS5	06cks5 kluyveromyc	1074	67	7.4	509	2	09LRJ1	09lrj1 triticum ae
1002	67.5	7.4	846	2	09C101	09c101 lactococcus	1075	67	7.4	535	2	P728J9	p728j9 synechocyst
1003	67.5	7.4	851	2	08L6J3	08l6j3 arabidopsis	1076	67	7.4	552	2	065XU0	065xu0 oryza sativ
1004	67.5	7.4	916	2	09YXK8	09yxk8 neiseeria m	1077	67	7.4	554	2	06NTE7	06nte7 homo sapien
1005	67.5	7.4	946	2	075QNG	075qng arabidopsis	1078	67	7.4	592	2	08ERD5	08erd5 oceanobacil
1006	67.5	7.4	946	2	09FFA8	09ffa8 arabidopsis	1079	67	7.4	600	2	07YZB8	07yzb8 tenebrio mo
1007	67.5	7.4	959	2	06FT79	06ft79 candida gla	1080	67	7.4	600	2	0701L8	0701l8 homo sapien
1008	67.5	7.4	989	2	023723	023723 arabidopsis	1081	67	7.4	613	2	06T721	06t721 brachydanio
1009	67.5	7.4	1005	2	093708	093708 escherichia	1082	67	7.4	618	2	093JN4	093jn4 xenotomonas
1010	67.5	7.4	1108	2	08I7E8	08i7e8 bacillus ce	1083	67	7.4	628	2	07UZR4	07uzr4 prochloroco
1011	67.5	7.4	1130	2	08CFE5	08cfe5 mus musculu	1084	67	7.4	629	1	Q7XV05	q7xv05 oryza sativ
1012	67.5	7.4	1138	2	022276	022276 caenorhabdi	1085	67	7.4	639	2	K2C3_HUMAN	k2c3_human
1013	67.5	7.4	1140	2	069ZW5	069zw5 mus musculu	1086	67	7.4	639	2	09SFE4	09sfe4 arabidopsis
1014	67.5	7.4	1191	1	CING_MOUSE	cing242 mus musculu	1087	67	7.4	634	2	094KAS	094kas picea abies
1015	67.5	7.4	1223	2	06P2K0	06p2k0 mus musculu	1088	67	7.4	639	2	09XHZ6	09xhz6 arabidopsis
1016	67.5	7.4	1240	2	069ZM0	069zm0 mus musculu	1089	67	7.4	671	2	07QJ04	07qj04 anopheles g
1017	67.5	7.4	1258	2	06BGB6	06bgb6 paramecium	1090	67	7.4	701	2	06A9K7	06a9k7 proflionbac
1018	67.5	7.4	1287	2	07Z362	07z362 homo sapien	1091	67	7.4	733	2	06BK65	06bk65 debaryomyce
1019	67.5	7.4	1509	2	07QOP8	07qop8 giardia lam	1092	67	7.4	790	2	06BJ29	06bj29 debaryomyce
1020	67.5	7.4	1572	2	06MJT8	06mjt8 bdellovibri	1093	67	7.4	824	2	09XJ26	09xj26 saccharomyc
1021	67.5	7.4	1624	2	09W4J7	09w4j7 drosophila	1094	67	7.4	833	2	08LJDO	08ljdo bacillus ce
1022	67.5	7.4	1964	2	093522	093522 xenopus lae	1095	67	7.4	844	2	086V65	086v65 homo sapien
1023	67.5	7.4	2077	2	06WMN2	06wmn2 neurospora	1096	67	7.4	856	2	06C9T4	06c9t4 oryza sativ
1024	67.5	7.4	3175	2	07JKT8	07jkt8 caenorhabdi	1097	67	7.4	857	2	08WV98	08wv98 homo sapien
1025	67.5	7.4	3184	2	09XV66	09xv66 caenorhabdi	1098	67	7.4	861	2	0887K8	0887k8 pseudomonas
1026	67.5	7.4	6885	1	SNE2_HUMAN	snex10 homo sapien	1099	67	7.4	872	2	08BO74	08bo74 m mus muscu
1027	67	7.4	118	2	064HN4	064hn4 bacterioph	1100	67	7.4	888	2	09P221	09p221 homo sapien
1028	67	7.4	118	2	064HN6	064hn6 bacterioph	1101	67	7.4	891	2	06BDH6	06bdh6 homo sapien
1029	67	7.4	153	2	073KS0	073ks0 treponema d	1102	67	7.4	928	1	NIBA_HUMAN	niba_human
1030	67	7.4	172	2	093VL3	093vl3 phaseolus v	1103	67	7.4	931	2	09SUX9	09sux9
1031	67	7.4	180	2	07XBY8	07xby8 oryza sativ	1104	67	7.4	941	2	09UXV7	09uxv7
1032	67	7.4	180	2	09AYL7	09ayl7 oryza sativ	1105	67	7.4	941	2	028662	028662
1033	67	7.4	207	1	RS4_BORPE	rs4b774 bordetella	1106	67	7.4	945	2	09TSL4	09tsl4
1034	67	7.4	234	1	B10D_BACSH	b10d818 bacillus sp	1107	67	7.4	945	2	06L465	06l465
1035	67	7.4	237	2	083LJ4	083lj4 shigella fl	1108	67	7.4	1008	2	08YQ48	08yq48 anabana ep
1036	67	7.4	264	2	022027	022027 caenorhabdi	1109	67	7.4	1047	2	066QA6	066qa6 oryza sativ
1037	67	7.4	266	2	06HMT2	06hmt2 bacillus an	1110	67	7.4	1066	1	SYI_PYRHO	syi_pyrho
1038	67	7.4	270	2	08D8F1	08d8f1 vibrio vuln	1111	67	7.4	1108	2	09PMD0	09pmd0
1039	67	7.4	283	2	08DA83	08da83 vibrio vuln	1112	67	7.4	1126	2	073ME8	073me8 treponema d
1040	67	7.4	287	2	08MRP1	08mr1 caenorhabdi	1113	67	7.4	1128	2	07SKZ2	07skz2 brachydanio
1041	67	7.4	293	2	066666	066666 aquilex aeo	1114	67	7.4	1154	2	068XK6	068xk6 ticketella
1042	67	7.4	303	2	08BHV4	08bhv4 mus musculu	1115	67	7.4	1158	2	086HX2	086hx2 dictyosteli
1043	67	7.4	316	2	06MBD7	06mbd7 parachlamyd	1116	67	7.4	1184	2	07VYV9	07vyv9 cryptocspori
1044	67	7.4	317	2	06JOY5	06joy5 parallelchth	1117	67	7.4	1235	1	KPB2_MOUSE	kpb2_mus musculu
1045	67	7.4	329	2	075JW2	075jw2 arabhya goos	1118	67	7.4	1241	1	KPB1_MOUSE	kpb1_mus musculu
1046	67	7.4	336	2	08WZL6	08wzl6 yarrowia li	1119	67	7.4	1242	2	0824R6	0824r6 chlamydomphi
1047	67	7.4	336	2	06C3B1	06c3b1 yarrowia li	1120	67	7.4	1278	2	050667	050667 borella bu
1048	67	7.4	365	2	079JBI	079jel corynebacte	1121	67	7.4	1283	2	08ISR4	08isr4 plasmodium
1049	67	7.4	365	2	08NTG4	08ntg4 corynebacte	1122	67	7.4	1292	2	06C9J0	06c9j0 yarrowia li
1050	67	7.4	391	2	097Y44	097y44 sulfolobus	1123	67	7.4	1632	2	084KC9	084kc9 hordeum vul
1051	67	7.4	410	2	07VJG7	07vjg7 haemophilus	1124	67	7.4	1739	2	06ZE11	06ze11 oryza sativ
1052	67	7.4	411	2	087JW8	087jw8 mucor circi	1125	67	7.4	1805	1	HMR2_MYCGE	hmr2_mycoplasma
1053	67	7.4	421	2	08XPJ5	08xpj5 ralteonria s	1126	67	7.4	1863	2	07XT09	07xt09 oryza sativ
										2094	2	080Y35	080y35 mus musculu

1127	67	7.4	2182	2	081125	081125 plasmodium	1200	66.5	7.3	875	2	Q723V3	Q723V3 homo sapien
1128	67	7.4	2527	2	095M83	095M83 plasmodium	1201	66.5	7.3	876	2	Q78B7	Q78B7 mus musculu
1129	67	7.4	3320	2	Q73MFO	Q73MFO treponema d	1202	66.5	7.3	880	1	TYO3_MOUSE	P55144 mus musculu
1130	67	7.4	4624	1	DYH5_HUMAN	Q8E73 homo sapien	1203	66.5	7.3	880	1	TYO3_RAT	P55146 ratu
1131	66.5	7.3	144	2	096MK1	Q96MK1 homo sapien	1204	66.5	7.3	880	1	Q6NZM6	Q6NZM6 mus musculu
1132	66.5	7.3	211	2	0608M4	Q608M4 uncultured	1205	66.5	7.3	885	1	VP39_HUMAN	Q661CI mus musculu
1133	66.5	7.3	264	2	08WVG2	Q8WVG2 homo sapien	1206	66.5	7.3	894	2	Q6DD73	Q6DD73 xenopus lae
1134	66.5	7.3	279	2	064UP9	Q64UP9 bacteroides	1207	66.5	7.3	916	2	Q9UTK7	Q9UTK7 neiseeria m
1135	66.5	7.3	287	2	064Y62	Q64Y62 bacteroides	1208	66.5	7.3	923	2	Q81Q88	Q81Q88 drosophila
1136	66.5	7.3	292	2	06ASA4	Q6ASA4 desulfotale	1209	66.5	7.3	950	2	Q95N26	Q95N26 dictyosteli
1137	66.5	7.3	303	2	081A70	Q81A70 bacillus ce	1210	66.5	7.3	960	2	Q81B26	Q81B26 bacillus ce
1138	66.5	7.3	333	2	Q7V472	Q7V472 prochloroco	1211	66.5	7.3	1037	2	Q6GL13	Q6GL13 xenopus tro
1139	66.5	7.3	341	2	Q73515	Q73515 bacillus ce	1212	66.5	7.3	1081	2	Q8BMA5	Q8BMA5 mus musculu
1140	66.5	7.3	342	2	Q7V432	Q7V432 prochloroco	1213	66.5	7.3	1108	2	Q72ZD3	Q72ZD3 bacillus ce
1141	66.5	7.3	350	2	Q7P8T5	Q7P8T5 anopheles g	1214	66.5	7.3	1110	2	Q9SUZ3	Q9SUZ3 arbidopais
1142	66.5	7.3	357	2	Q96D17	Q96D17 homo sapien	1215	66.5	7.3	1121	2	Q7QXJ5	Q7QXJ5 giardia lam
1143	66.5	7.3	358	2	06P801	Q6P801 mus musculu	1216	66.5	7.3	1128	2	Q7UDB4	Q7UDB4 shigella fl
1144	66.5	7.3	360	2	064BP4	Q64BP4 uncultured	1217	66.5	7.3	1195	2	Q9C730	Q9C730 arbidopais
1145	66.5	7.3	362	2	08A7L9	Q8A7L9 bacteroides	1218	66.5	7.3	1198	2	Q6FDP6	Q6FDP6 actinobact
1146	66.5	7.3	381	2	Q8NEY4	Q8NEY4 homo sapien	1219	66.5	7.3	1246	2	Q9C6Q9	Q9C6Q9 arbidopais
1147	66.5	7.3	381	2	Q96EL8	Q96EL8 homo sapien	1220	66.5	7.3	1260	2	Q65XW3	Q65XW3 oryza sativ
1148	66.5	7.3	382	1	TGT_HAETIN	Q8EHX2 pseudomonas	1221	66.5	7.3	1363	2	Q65XW3	Q65XW3 oryza sativ
1149	66.5	7.3	392	1	Q8TQ4	Q8TQ4 haemophilus	1221	66.5	7.3	1504	2	Q9LKH4	Q9LKH4 arbidopais
1150	66.5	7.3	401	2	Q75B77	Q75B77 aabhyra goss	1222	66.5	7.3	1728	2	Q9LU12	Q9LU12 arbidopais
1151	66.5	7.3	406	2	Q9FJ17	Q9FJ17 arbidopais	1223	66.5	7.3	1833	2	Q80T68	Q80T68 mus musculu
1152	66.5	7.3	412	2	Q8AVX9	Q8AVX9 xenopus lae	1224	66.5	7.3	1976	1	MYHA_BOVIN	Q27991 bos taurus
1153	66.5	7.3	428	2	Q6P8E8	Q6P8E8 xenopus lae	1225	66.5	7.3	2202	2	Q6BPL1	Q6BPL1 debaryomyce
1154	66.5	7.3	433	2	Q52160	Q52160 plasmid pres	1226	66.5	7.3	2217	2	Q6FNV7	Q6FNV7 candida gla
1155	66.5	7.3	439	2	Q8YK82	Q8YK82 anabaena sp	1227	66.5	7.3	119	2	Q9XZ82	Q9XZ82 plasmodium
1156	66.5	7.3	439	2	Q7U3J0	Q7U3J0 synechococc	1228	66.5	7.3	158	2	Q8YVB0	Q8YVB0 anabaena sp
1157	66.5	7.3	446	2	Q8VXD4	Q8VXD4 nicotiana t	1229	66.5	7.3	160	1	COAD_CONGL	Q8VXD4 cornehyne
1158	66.5	7.3	446	2	Q8ST97	Q8ST97 nicotiana t	1230	66.5	7.3	177	2	Q726E0	Q726E0 bean dwarf
1159	66.5	7.3	455	2	Q88HX2	Q88HX2 pseudomonas	1231	66.5	7.3	180	2	Q6S941	Q6S941 plasmodium
1160	66.5	7.3	485	2	Q80401	Q80401 oryza sativ	1232	66.5	7.3	208	2	Q7PMQ3	Q7PMQ3 anopheles g
1161	66.5	7.3	494	1	WD37_HUMAN	Q9Y218 homo sapien	1233	66.5	7.3	210	2	Q8VTP2	Q8VTP2 helicobacte
1162	66.5	7.3	513	1	VGA_BPPIX	P33631 bacterioph	1234	66.5	7.3	210	2	Q8VTP3	Q8VTP3 helicobacte
1163	66.5	7.3	523	2	Q71A13	Q71A13 anaplasma m	1235	66.5	7.3	214	1	Y629_MERTU	Q69356 methanococc
1164	66.5	7.3	534	1	YF84_STR6	P67283 streptococc	1236	66.5	7.3	234	2	Q49351	Q49351 arbidopais
1165	66.5	7.3	534	1	YH39_STRPN	P67282 streptococc	1237	66.5	7.3	237	2	Q9KEH9	Q9KEH9 bacillus ha
1166	66.5	7.3	562	1	YH39_STRPN	Q95046 trypanosoma	1238	66.5	7.3	248	2	Q937X0	Q937X0 sphingomyca
1167	66.5	7.3	563	1	YWO3_CAEEL	Q10906 caenorhabdi	1239	66.5	7.3	258	2	Q53736	Q53736 synechocyst
1168	66.5	7.3	568	2	Q6CAH0	Q6CAH0 varicowia li	1240	66.5	7.3	259	2	Q41533	Q41533 triticum ae
1169	66.5	7.3	575	2	Q6DD66	Q6DD66 erwinita car	1241	66.5	7.3	270	2	Q7MM15	Q7MM15 vibrio vuln
1170	66.5	7.3	581	2	Q6EBB6	Q6EBB6 campylobact	1242	66.5	7.3	277	2	Q847U9	Q847U9 vibrio para
1171	66.5	7.3	597	2	Q91871	Q91871 xenopus lae	1243	66.5	7.3	277	2	Q87GA7	Q87GA7 vibrio para
1172	66.5	7.3	600	2	Q9PHM8	Q9PHM8 campylobact	1244	66.5	7.3	287	2	Q9XX63	Q9XX63 caenorhabdi
1173	66.5	7.3	608	2	Q6O378	Q6O378 homo sapien	1245	66.5	7.3	289	2	Q7QBR3	Q7QBR3 anopheles g
1174	66.5	7.3	608	2	Q6KJ38	Q6KJ38 oryza sativ	1246	66.5	7.3	332	2	Q8VMK6	Q8VMK6 pseudomonas
1175	66.5	7.3	629	2	Q94HJ4	Q94HJ4 oryza sativ	1247	66.5	7.3	332	2	Q8VUH7	Q8VUH7 pseudomonas
1176	66.5	7.3	633	2	Q9H094	Q9H094 homo sapien	1248	66.5	7.3	332	2	Q88117	Q88117 pseudomonas
1177	66.5	7.3	636	2	Q35656	Q35656 mus musculu	1249	66.5	7.3	337	2	Q9MWY4	Q9MWY4 pseudomonas
1178	66.5	7.3	641	2	Q8WMT4	Q8WMT4 homo sapien	1250	66.5	7.3	340	1	PFTA_ARATH	Q9WVY4 pseudomonas
1179	66.5	7.3	643	2	Q6P3X9	Q6P3X9 homo sapien	1251	66.5	7.3	344	1	Q6C6W3	Q6C6W3 a proteain f
1180	66.5	7.3	652	2	Q8IM59	Q8IM59 plasmodium	1252	66.5	7.3	361	2	Q6AGP6	Q6AGP6 yarrowia li
1181	66.5	7.3	658	2	Q63116	Q63116 bacillus ce	1253	66.5	7.3	363	2	Q98321	Q98321 leifsonia x
1182	66.5	7.3	658	2	Q72XV1	Q72XV1 bacillus ce	1254	66.5	7.3	374	2	Q8BCK3	Q8BCK3 hyemasprien
1183	66.5	7.3	658	2	Q81513	Q81513 bacillus ce	1255	66.5	7.3	375	1	TGT_ECOLI	QECMA3 shewanella
1184	66.5	7.3	658	2	Q81X47	Q81X47 bacillus an	1256	66.5	7.3	375	1	TGT_SHIFL	P19675 escherichia
1185	66.5	7.3	658	2	Q6HBC2	Q6HBC2 bacillus th	1257	66.5	7.3	375	2	Q8RB71	Q8RB71 shigella fl
1186	66.5	7.3	666	2	Q64XN8	Q64XN8 bacteroides	1258	66.5	7.3	386	2	Q83V39	Q83V39 pseudomonas
1187	66.5	7.3	666	2	Q6HP67	Q6HP67 bacteroides	1259	66.5	7.3	399	2	Q21342	Q21342 xenophorabi
1188	66.5	7.3	679	2	Q8EB85	Q8EB85 bacillus th	1260	66.5	7.3	414	2	Q36857	Q36857 xiphopteris
1189	66.5	7.3	681	2	Q8KPY1	Q8KPY1 synechococc	1261	66.5	7.3	424	2	Q6AUC7	Q6AUC7 desulfotale
1190	66.5	7.3	694	2	Q6DE20	Q6DE20 xenopus lae	1262	66.5	7.3	434	1	Q9LJ36	Q9LJ36 anabaena sp
1191	66.5	7.3	735	2	Q8WGU6	Q8WGU6 pennantia c	1263	66.5	7.3	437	1	LH2A_HUMAN	Q00534 homo sapien
1192	66.5	7.3	745	2	Q6PCF2	Q6PCF2 xenopus lae	1264	66.5	7.3	467	2	Q6GR24	Q6GR24 xenopus lae
1193	66.5	7.3	763	2	Q8WWS6	Q8WWS6 homo sapien	1265	66.5	7.3	470	2	P94053	Q94053 plocama pen
1194	66.5	7.3	771	2	Q9BVV6	Q9BVV6 homo sapien	1266	66.5	7.3	475	2	Q8HW61	Q8HW61 sematophylli
1195	66.5	7.3	793	2	Q84TB4	Q84TB4 oryza sativ	1267	66.5	7.3	475	2	Q33631	Q33631 streptococc
1196	66.5	7.3	832	1	TRNL_CANAL	P43075 candida alb	1268	66.5	7.3	479	2	Q8EAB9	Q8EAB9 shewanella
1197	66.5	7.3	837	2	Q6PB65	Q6PB65 mus musculu	1269	66.5	7.3	492	1	K2CO_CHICK	Q93532 gallus gall
1198	66.5	7.3	867	2	Q81210	Q81210 arabidopsis	1270	66.5	7.3	498	2	Q6CZD8	Q6CZD8 erwinita car
1199	66.5	7.3	875	2	Q71S06	Q71S06 homo sapien	1271	66.5	7.3	499	1	NIFB_BRAJA	P65770 bradyrhizob
							1272	66.5	7.3	503	2	Q95LVO	Q95LVO macaca fasc

1273	66	7.3	514	2	Q80VD9	Q80vd9 mus musculus	1346	65.5	7.2	206	1	RS4_PHOIL	Q7myh4 photorhabdu
1274	66	7.3	540	2	Q6MFA7	Q6mfar parachlamy	1347	65.5	7.2	206	2	Q65OX9	Q65gx9 manheimia
1275	66	7.3	553	2	Q9KC39	Q9kcx9 bacillus ha	1348	65.5	7.2	223	2	Q6PH25	Q6ph25 brachydanio
1276	66	7.3	554	2	Q36X04	Q36x04 podospora a	1349	65.5	7.2	228	2	Q83CF9	Q83cf9 enterococu
1277	66	7.3	562	1	EZRA_BACSU	Q34894 bacillus su	1350	65.5	7.2	249	1	PSB2_THETN	Q8r912 thermaner
1278	66	7.3	566	2	Q7X3P9	Q7x3p9 staphylococ	1351	65.5	7.2	252	2	Q99V78	Q99v78 staphylococ
1279	66	7.3	573	2	Q6E1N1	Q6e1n1 bacillus sp	1352	65.5	7.2	252	2	Q7A199	Q7a199 staphylococ
1280	66	7.3	573	2	Q6E1N6	Q6e1n6 geobacillus	1353	65.5	7.2	252	2	Q7A6D5	Q7a6d5 staphylococ
1281	66	7.3	575	2	Q6P6Q2	Q6p6q2 rattus norv	1354	65.5	7.2	252	2	Q6GAR3	Q6gar3 staphylococ
1282	66	7.3	576	2	Q6P6Q2	Q6p6q2 rattus norv	1355	65.5	7.2	256	2	Q8C3X2	Q8c3x2 mus musculu
1283	66	7.3	576	2	Q6P6Q2	Q6p6q2 rattus norv	1356	65.5	7.2	256	2	Q9D7C1	Q9d7c1 mus musculu
1284	66	7.3	600	2	Q9ET74	Q9et74 mus musculu	1357	65.5	7.2	285	2	Q6DEA2	Q6dea2 xenopus lae
1285	66	7.3	644	2	Q73E11	Q73e11 bacillus ce	1358	65.5	7.2	289	2	Q75BV1	Q75bv1 ashbya gos
1286	66	7.3	660	2	Q6F9S7	Q6f9s7 acinetobact	1359	65.5	7.2	289	2	Q8A6H6	Q8a6h6 bacteroides
1287	66	7.3	685	2	Q8D4E5	Q8d4e5 vibrio vuln	1360	65.5	7.2	300	1	SP18_YEAST	P32572 saccharomyc
1288	66	7.3	716	2	Q7MP22	Q7mp22 vibrio vuln	1361	65.5	7.2	328	1	AIPL_MOUSE	Q924k1 mus musculu
1289	66	7.3	729	1	PCRA_STAEP	Q8cte8 staphylococ	1362	65.5	7.2	332	2	Q8Q5S3	Q8qes3 human immun
1290	66	7.3	730	2	Q87JC8	Q87jce8 neurospora	1363	65.5	7.2	333	2	Q8KSX2	Q8ksx2 streptomyce
1291	66	7.3	781	2	Q6NUJ2	Q6nuj2 xenopus lae	1364	65.5	7.2	351	2	Q8Z2S0	Q8z2s0 salmonella
1292	66	7.3	786	1	STSB_MOUSE	P42232 mus musculu	1365	65.5	7.2	351	2	Q8ZLF0	Q8zlf0 salmonella
1293	66	7.3	786	1	STSB_RAT	P52632 rattus norv	1366	65.5	7.2	353	2	Q6ZRL4	Q6zrl4 homo sapien
1294	66	7.3	786	2	Q8K3Q1	Q8k3q1 mus sapien	1367	65.5	7.2	354	1	YBBB_ECOLI	P33667 escherichia
1295	66	7.3	786	2	Q9UKM1	Q9ukm1 mus musculu	1368	65.5	7.2	364	2	Q8XC22	Q8xc22 escherichia
1296	66	7.3	791	2	Q8WMS9	Q8wms9 homo sapien	1369	65.5	7.2	366	2	Q7Q0Z1	Q7q0z1 anopheles g
1297	66	7.3	794	1	STSA_HUMAN	P42229 homo sapien	1370	65.5	7.2	371	2	Q6E130	Q6e130 synechococc
1298	66	7.3	799	2	Q6BLI8	Q6bli8 debaryomyce	1371	65.5	7.2	372	2	Q93Q33	Q93q33 salmonella
1299	66	7.3	805	2	Q6RK13	Q6rk13 parietaria	1372	65.5	7.2	372	2	Q455Q6	Q455q6 bacillus su
1300	66	7.3	812	2	Q9AC93	Q9acg3 oryza sativ	1373	65.5	7.2	375	2	Q9S522	Q9s522 escherichia
1301	66	7.3	816	2	Q9C9H7	Q9c9h7 arabidopsis	1374	65.5	7.2	375	1	TGT_SALTI	Q828y0 salmonella
1302	66	7.3	846	2	Q9PN76	Q9pn76 campylobact	1375	65.5	7.2	375	2	Q97EW2	Q97ew2 clostridium
1303	66	7.3	853	1	PHS1_DICDI	Q00766 dictyosteli	1376	65.5	7.2	377	2	Q72U33	Q72u33 leptospira
1304	66	7.3	867	2	Q6AXB4	Q6axb4 mus musculu	1377	65.5	7.2	378	2	Q8YUM5	Q8yum5 anabaena sp
1305	66	7.3	922	2	Q8TCV9	Q8tcv9 homo sapien	1378	65.5	7.2	380	2	Q63QX3	Q63qx3 burkholderi
1306	66	7.3	1018	2	Q9HCT1	Q9hct1 homo sapien	1379	65.5	7.2	384	2	Q7QKN1	Q7qkn1 anopheles g
1307	66	7.3	1028	2	Q6IR24	Q6ir24 onion yellu	1380	65.5	7.2	387	2	Q9X941	Q9x941 streptomyce
1308	66	7.3	1031	1	KINH_STRPU	P35978 strongyloce	1381	65.5	7.2	404	1	FGK_MYCNS	P62415 mycoplasma
1309	66	7.3	1047	1	Q67IT5	Q67it5 oryza sativ	1382	65.5	7.2	405	2	Q9M2V1	Q9m2v1 arabidopsis
1310	66	7.3	1050	1	HER3_HUMAN	Q15034 homo sapien	1383	65.5	7.2	424	2	Q8B6C5	Q8b6c5 pseudomonas
1311	66	7.3	1052	2	Q91G49	Q91g49 chilo tride	1384	65.5	7.2	430	1	FOLC_BACSU	Q09400 caenorhabdi
1312	66	7.3	1099	2	Q6FV36	Q6fv36 candida gla	1385	65.5	7.2	431	1	SGK1_RABIT	Q05865 bacillus su
1313	66	7.3	1160	2	Q6NX72	Q6nx72 homo sapien	1386	65.5	7.2	431	2	Q8V3V9	Q8v3v9 cryptococcus
1314	66	7.3	1181	2	Q9KN45	Q9kn45 vibrio chol	1387	65.5	7.2	446	2	Q8VD23	Q8vd23 mus musculu
1315	66	7.3	1199	2	Q8NMW7	Q8nmw7 homo sapien	1388	65.5	7.2	451	2	Q89VS8	Q89v8 bradyrhizob
1316	66	7.3	1274	2	Q8NFR0	Q8nfr0 homo sapien	1389	65.5	7.2	463	1	YRB3_CABEL	Q09408 caenorhabdi
1317	66	7.3	1289	2	Q62T17	Q62t17 rattus norv	1390	65.5	7.2	465	2	Q9U1S3	Q9u1s3 caenorhabdi
1318	66	7.3	1318	2	Q6FTJ2	Q6ftj2 candida gla	1391	65.5	7.2	471	2	Q85YMO	Q85ymo monadenium
1319	66	7.3	1336	2	Q7R3R6	Q7r3r6 giardia lam	1392	65.5	7.2	483	2	Q7NIG0	Q7nig0 gloeobacter
1320	66	7.3	1382	2	Q61374	Q61374 mus musculu	1393	65.5	7.2	494	2	Q63G58	Q63g58 bacillus ce
1321	66	7.3	1383	2	Q9VDA0	Q9vda0 drosophila	1394	65.5	7.2	486	2	Q8FHD0	Q8fhd0 escherichia
1322	66	7.3	1390	2	Q9UL08	Q9ul08 homo sapien	1395	65.5	7.2	486	2	Q83RE9	Q83re9 shigella fl
1323	66	7.3	1392	2	Q80TV1	Q80tv1 mus musculu	1396	65.5	7.2	496	2	Q8Y649	Q8y649 listeria mo
1324	66	7.3	1610	2	Q74349	Q74349 echizosacch	1397	65.5	7.2	509	2	Q7UHA1	Q7uha1 rhodospirell
1325	66	7.3	1732	2	Q7QDL1	Q7qdl1 anopheles g	1398	65.5	7.2	531	2	Q7Y205	Q7y205 cryptospori
1326	66	7.3	1953	1	BN11_YEAST	P41832 saccharomyc	1399	65.5	7.2	540	2	Q8D8W2	Q8d8w2 vibrio vuln
1327	66	7.3	2013	1	Q9VK10	Q9vki0 drosophila	1400	65.5	7.2	542	2	Q7MLD0	Q7ml0 vibrio vuln
1328	66	7.3	2090	1	NIN_HUMAN	Q9n4c6 homo sapien	1401	65.5	7.2	543	2	Q9QO15	Q9qo15 influenza a
1329	66	7.3	2244	2	Q9NCG0	Q9ncg0 drosophila	1402	65.5	7.2	545	2	Q88B36	Q88b36 mus musculu
1330	66	7.3	2282	2	Q6CAD2	Q6cad2 yarrowia li	1403	65.5	7.2	566	2	Q6ZTE7	Q6zte7 mus musculu
1331	66	7.3	2326	2	Q81IV6	Q81iv6 plasmodium	1404	65.5	7.2	566	2	Q32239	Q32239 bacillus su
1332	66	7.3	2524	1	NOTC_XENLA	P17183 xenopus lae	1405	65.5	7.2	569	2	Q8LW96	Q8lwn9 oryza sativ
1333	66	7.3	3265	2	Q81D63	Q81d63 plasmodium	1406	65.5	7.2	576	2	Q83SE9	Q83se9 shigella fl
1334	66	7.3	4264	2	Q7PPJ1	Q7ppj1 anopheles g	1407	65.5	7.2	600	2	Q91ZJ7	Q91zj7 mus musculu
1335	66	7.2	114	2	Q8T327	Q8t327 plasmodium	1408	65.5	7.2	621	2	Q6NSU0	Q6nsu0 mus musculu
1336	65.5	7.2	126	2	Q9MZF8	Q9mzf8 mecaca mula	1409	65.5	7.2	624	2	Q6S7P1	Q6s7p1 oryza sativ
1337	65.5	7.2	151	2	Q6S8V1	Q6s8v1 plasmodium	1410	65.5	7.2	624	2	Q6Z4U4	Q6z4u4 oryza sativ
1338	65.5	7.2	170	2	Q6H1E8	Q6h1e8 bacillus th	1411	65.5	7.2	626	2	Q81RB3	Q81rb3 drosophila
1339	65.5	7.2	182	2	Q67BJ6	Q67bj6 ovine herpe	1412	65.5	7.2	664	2	Q7RR19	Q7rr19 plasmodium
1340	65.5	7.2	183	2	Q8DWM7	Q8dwm7 streptococc	1413	65.5	7.2	677	2	Q7ZBN0	Q7zbn0 desulfovibr
1341	65.5	7.2	183	2	Q8E2R8	Q8e2r8 streptococc	1414	65.5	7.2	689	2	P87565	P87565 canine aden
1342	65.5	7.2	199	2	Q8R5O5	Q8r5o5 mus musculu	1415	65.5	7.2	694	2	Q751Y8	Q751y8 ashbya gos
1343	65.5	7.2	205	1	RS4_HAEIN	P44373 haemophilus	1416	65.5	7.2	706	2	Q8BKB3	Q8bkb3 mus musculu
1344	65.5	7.2	206	1	RS4_BUCBP	P59491 buchiera ap	1417	65.5	7.2	716	2	Q7QK23	Q7qk23 anopheles g
1345	65.5	7.2	206	1	RS4_PASMU	Q9c153 pasteurella	1418	65.5	7.2	745	1	CUL2_HUMAN	Q13617 homo sapien

1419	65.5	7.2	745	1	CUL2, MOUSE	O6q4h8	mus musculus
1420	65.5	7.2	756	2	O69D70	O6q4d0	Oryza sativ
1421	65.5	7.2	777	2	O81G16	O81G96	Bacillus ce
1422	65.5	7.2	798	2	O8BUJ2	O8BUJ2	mus musculus
1423	65.5	7.2	803	2	O9CB85	O9CB85	mycobacteri
1424	65.5	7.2	811	2	O6G1O8	O6G1O8	bartonella
1425	65.5	7.2	821	2	P72351	P72351	mycobacteri
1426	65.5	7.2	826	2	O6FPN1	O6FPN1	actinobact
1427	65.5	7.2	845	1	AMPN_LALIC	P37897	lactococcus
1428	65.5	7.2	875	2	O8BY36	O8BY36	mus musculus
1429	65.5	7.2	886	1	VP39, MOUSE	O8r513	mus musculus
1430	65.5	7.2	913	2	O12151	O12151	saccharomyc
1431	65.5	7.2	932	2	O9CEH8	O9ceh8	lactococcus
1432	65.5	7.2	940	2	O35157	O35157	mus musculus
1433	65.5	7.2	944	2	O829N2	O829n2	salmonella
1434	65.5	7.2	944	2	O82R20	O82r20	salmonella
1435	65.5	7.2	958	2	O68FLO	O68f10	mus musculus
1436	65.5	7.2	969	2	O8N3W0	O8n3w0	homo sapien
1437	65.5	7.2	970	1	NAO1, MOUSE	P70414	mus musculus
1438	65.5	7.2	983	2	O9QXN1	O9qxm1	mus musculus
1439	65.5	7.2	988	2	O8GTB2	O8gtb2	homo sapien
1440	65.5	7.2	1012	2	O6CYH4	O6cyh4	kluyveromyc
1441	65.5	7.2	1013	2	O85920	O85920	spingomona
1442	65.5	7.2	1015	2	O8YVPA	O8yvda	anabaena sp
1443	65.5	7.2	1038	2	O7OD58	O7qds8	anopheles g
1444	65.5	7.2	1060	2	O7ZX11	O7zx11	xenopus lae
1445	65.5	7.2	1061	2	O69YK7	O69yk7	homo sapien
1446	65.5	7.2	1063	2	O81WFA	O81wf4	homo sapien
1447	65.5	7.2	1063	2	O8N4O6	O8n4o6	homo sapien
1448	65.5	7.2	1088	2	O00905	O00905	oxytricha f
1449	65.5	7.2	1115	2	O17267	O17267	caenorhabdi
1450	65.5	7.2	1130	2	O81TY8	O81ty8	caenorhabdi
1451	65.5	7.2	1133	2	O81949	O81949	anopheles g
1452	65.5	7.2	1153	2	O6B1P2	O6b1p2	debaromyce
1453	65.5	7.2	1157	2	O897P5	O897p5	clostridium
1454	65.5	7.2	1164	1	TSO1, HUMMAN	O92574	homo sapien
1455	65.5	7.2	1186	2	O6FW19	O6fw19	homo sapien
1456	65.5	7.2	1197	2	O9B121	O9b121	candida gla
1457	65.5	7.2	1197	2	O9VCH8	O9vch8	drosophila
1458	65.5	7.2	1203	2	O6PFK8	O6pfk8	brachydanio
1459	65.5	7.2	1204	2	O75A42	O75a42	anopheles goss
1460	65.5	7.2	1227	2	O7O0K7	O7o0k7	anopheles g
1461	65.5	7.2	1275	2	O6Z3S5	O6z3s5	oryza sativ
1462	65.5	7.2	1415	2	O9HCP4	O9hcf4	homo sapien
1463	65.5	7.2	1487	1	NUKB_VIBPA	O8tqw2	vibrio para
1464	65.5	7.2	1509	2	O6MBY1	O6mbyl	parachlamyd
1465	65.5	7.2	1681	2	O9N8T7	O9n8t7	typanosoma
1466	65.5	7.2	1785	2	O6ZP10	O6zpl0	mus musculus
1467	65.5	7.2	1866	1	VGNB, CPWV	P03600	cowpea mosa
1468	65.5	7.2	2101	2	O14981	O14981	homo sapien
1469	65.5	7.2	2115	1	NIMA, HUMMAN	O14980	homo sapien
1470	65.5	7.2	2296	2	O75O42	O75o42	homo sapien
1471	65.5	7.2	3139	2	O9GM99	O9gm99	sus scrofa
1472	65.5	7.2	3152	2	O8U237	O8u237	leek yellow
1473	65.5	7.2	3397	2	O8UW79	O8uw79	gallus galli
1474	65.5	7.2	4390	2	O9VZ77	O9vz77	drosophila
1475	65.5	7.2	5229	2	O7RTF4	O7rtf4	plasmodium
1476	65.5	7.2	104	2	O79Y28	O79y28	streptococc
1477	65.5	7.2	105	2	O880J3	O880j3	pseudomonas
1478	65.5	7.2	156	2	O9FN29	O9fn29	arabidopsis
1479	65.5	7.2	157	2	O8RGJ3	O8rgj3	thermoanaer
1480	65.5	7.2	159	2	O9O3O8	O9o3o8	cotton yell
1481	65.5	7.2	190	2	O8WTD8	O8wtd8	plasmodium
1482	65.5	7.2	206	2	O7NBT7	O7nbt7	mycoplasma
1483	65.5	7.2	210	1	THAI, MOUSE	O8chw1	mus musculus
1484	65.5	7.2	210	1	O9PBE8	O9pbe8	helicobacte
1485	65.5	7.2	220	1	KAD, PYRAB	O9znz1	pyrococcus
1486	65.5	7.2	221	2	O7TF12	O7tf12	tritus cyto
1487	65.5	7.2	222	2	O9LWV6	O9lwv6	arabidopsis
1488	65.5	7.2	232	2	O841W5	O841w5	streptomyce
1489	65.5	7.2	236	2	O46Z48	O46z48	clostridium
1490	65.5	7.2	240	2	O8NKK5	O8nkk5	uncultured
1491	65.5	7.2	240	2	O8NKK5	O8nkk5	uncultured

1492	65	7.2	251	2	O8QMH8	O8qmh8	sida motile
1493	65	7.2	251	2	O70PC3	O70pc3	sida micran
1494	65	7.2	254	2	O913O7	O913o7	ragia cateab
1495	65	7.2	265	2	O6Y217	O6y217	paprus majo
1496	65	7.2	277	2	O7PSO9	O7ps09	anopheles g
1497	65	7.2	280	2	O25846	O25846	plasmodium
1498	65	7.2	280	2	O25855	O25855	plasmodium
1499	65	7.2	291	2	O8PV67	O8pv67	methanosarc
1500	65	7.2	291	2	O63HM6	O63hm6	homo sapien

ALIGNMENTS

RESULT 1
INT1 SHEEP
AC P56828; P08316;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interferon tau-1 precursor (IFN-tau) (Trophoblast protein-1) (TP-1) (Trophoblastin) (Antileucolysin) (Trophoblast antileucolytic protein).
GN Name=IFNT1; Synonyms=OTF;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Trophoblast;
RX MEDLINE=8806585; PubMed=2446135; DOI=10.1038/330377a0;
RA Imakawa K., Antony R.V., Kazemi M., Marotti K.R., Polites H.G.,
RA Roberts R.M.;
RT "Interferon-like sequence of ovine trophoblast protein secreted by embryonic trophoblastern";
RL Nature 330:377-379(1987).
RN [2]
RP FUNCTION.
RX MEDLINE=96174804; PubMed=8603586; DOI=10.1210/en.137.3.1144;
RA Spencer T.E., Bazer F.W.;
RT "Ovine interferon tau suppresses transcription of the estrogen receptor and oxytocin receptor genes in the ovine endometrium";
RL Endocrinology 137:1144-1147(1996).
RN [3]
RP CIRCULAR DICHOISM ANALYSIS, AND 3D-STRUCTURE MODELING.
RX MEDLINE=95062134; PubMed=7971949;
RA Jarpe M.A., Johnson H.M., Bazer F.W., Ott T.L., Curto E.V.,
RA Krishna N.R., Pontzer C.H.;
RT "Predicted structural motif of IFN tau";
RL Protein Eng. 7:863-867(1994).
RN [4]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=96318252; PubMed=8746786;
RA Senda T., Saitoh S.-I., Mitsui Y., Li J., Roberts R.M.;
RT "A three-dimensional model of interferon-tau";
RL J. Interferon Cytokine Res. 15:1053-1060(1995).
RN [5]
RP REVIEW.
RX MEDLINE=99081096; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
RA Martal J.-U., Chene N.M., Huynh L.P., V'Hardon R.M., Reinhard P.B.,
RA Guillomot M.W., Charlier M.A., Charpigny S.Y.;
RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-ubiquitous expression, structure-function relationships, a pregnancy hormonal embryonic signal and cross-species therapeutic potentialities";
RL Biochimie 80:755-777(1998).
CC -i- FUNCTION: Placental hormone primarily responsible for maternal recognition of pregnancy. Interacts with endometrial receptors, probably type I interferon receptors, and blocks estrogen receptor expression, preventing the estrogen-induced increase in oxytocin receptor expression in the endometrium. This results in the

suppression of the pulsatile endometrial release of the luteolytic hormone prostaglandin F2-alpha, hindering the regression of the corpus luteum (luteolysis) and therefore a return to ovarian cyclicity. This, and a possible direct effect of IFN-tau on prostaglandin synthesis, leads in turn to continued ovarian progesterone secretion, which stimulates the secretion by the endometrium of the nutrients required for the growth of the conceptus. In summary, displays particularly high antiviral and antiproliferative potency concurrently with particular weak cytotoxicity, high antiluteolytic activity and immunomodulatory properties. In contrast with other IFNs, IFN-tau is not virally inducible.

-1- SUBCELLULAR LOCATION: Secreted into the uterine lumen.

-1- TISSUE SPECIFICITY: Constitutively and exclusively expressed in the mononuclear cells of the extra-embryonic trophoderm.

-1- DEVELOPMENTAL STAGE: Major secretory product synthesized by the sheep conceptus between days 13 and 21 of pregnancy.

-1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from IFN-omega genes in the ruminantia suborder and have continued to duplicate independently in different lineages of the ruminantia. They encode for proteins very similar in sequence but with different biological potency and pattern of expression.

-1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-alpha1 subfamily.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.1sb-sib.ch/announce/> or send an email to license@1sb-sib.ch).

CC EMBL: Y00287; CA68396.1; -.

DR PIR: S03799; J50204.

DR PDB: 1BSL; X-ray; @=24-195.

DR InterPro: IPR005079; 4_helix_cytokine.

DR InterPro: IPR000471; Interferon_abd.

DR Pfam: PF00143; Interferon: 1.

DR PRINTS: PR00266; INTERFERONAB.

DR PRODOM: PD000550; Interferon_abd. 1.

DR PROSITE: PS00252; INTERFERON_A_B_D; 1.

KW 3D-structure; Antiviral; Cytokine; Hormone; Multigene family;

KW Pregnancy; Signal.

FT SIGNAL 1 23 By similarity.

FT CHAIN 1 195 Interferon tau-1.

FT DISULFID 24 122 By similarity.

FT DISULFID 52 162 By similarity.

FT TURN 25 26

FT HELIX 27 46

FT HELIX 47 47

FT TURN 47 47

FT HELIX 63 63

FT TURN 64 68

FT TURN 69 69

FT HELIX 73 95

FT TURN 96 97

FT TURN 100 101

FT HELIX 103 122

FT HELIX 138 136

FT TURN 157 159

FT HELIX 161 186

SO SEQUENCE 195 AA; 22192 MW; A495AE25DEA5BC9 CRC64;

Query Match 100.0%; Score 907; DB 1; Length 195;

Best Local Similarity 100.0%; Pred. No. 3.3e-76;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENLKLLDRNRRLSPSCQDRKDFGLPQENVGSDLOKQDAFPVLYEM 60

DB 24 CYLSRKMLDARENLKLLDRNRRLSPSCQDRKDFGLPQENVGSDLOKQDAFPVLYEM 83

QY 61 LQGSFNLFTYEHSSAAMDITLLBQLCTGLQOQLDHLDTGCGQVGEDESLGNMDPIVTV 120

DB 84 LQGSFNLFTYEHSSAAMDITLLBQLCTGLQOQLDHLDTGCGQVGEDESLGNMDPIVTV 143

QY 121 KKYFQGIYDYLQKGYSDCAWEIVRYEMRALVSTLQRLTKMGDLSNP 172

DB 144 KKYFQGIYDYLQKGYSDCAWEIVRYEMRALVSTLQRLTKMGDLSNP 195

RESULT 2

INT2 SHEEP STANDARD; PRT; 195 AA.

AC P56829; P08316;

DT 01-AUG-1988 (Rel. 08, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 05-JUN-2004 (Rel. 44, Last annotation update)

DE Interferon tau-2 precursor (IFN-tau2) (Trophoblast protein-1) (TP-1) (Trophoblastin) (Antiluteolysin) (Trophoblast antiluteolytic protein).

GN Name=IFNT2;

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Caprinae; Ovis.

OC NCBI_TaxID=9940;

RN [1]

RX SEQUENCE FROM N.A. (IFN-TAU2C).

RX MEDLINE=90040431; PubMed=2530342;

RA Stewart H.J., Flint A.P., Lamming G.E., McCann S.H., Parkinson T.J.;

RT "Antiluteolytic effects of blastocyst-secreted interferon investigated in vitro and in vivo in the sheep.";

RL J. Reprod. Fertil. Suppl. 37:127-138 (1989).

RN [2]

RX SEQUENCE FROM N.A. (IFN-TAU2C).

RX MEDLINE=89351557; PubMed=2475129;

RA Stewart H.J., McCann S.H., Northrop A.J., Lamming G.E., Flint A.P.;

RT "Sheep antiluteolytic interferon: cDNA sequence and analysis of mRNA levels.";

RL J. Mol. Endocrinol. 2:65-70 (1989).

RN [3]

RX SEQUENCE FROM N.A. (IFN-TAU2C).

RC TISSUE=Embryo;

RX MEDLINE=89326151; PubMed=2753362; DOI=10.1016/0378-1119(89)90082-6;

RA Charlier M., Hue D., Marcal J., Gaye P.;

RT "Cloning and expression of cDNA encoding ovine trophoblastin: its identity with a class-II alpha interferon.";

RL Gene 77:341-346 (1989).

RN [4]

RX SEQUENCE FROM N.A. (IFN-TAU2C).

RX MEDLINE=91067497; PubMed=1701245;

RA Klemann S.W., Imakawa K., Roberts R.M.;

RT "Sequence variability among ovine trophoblast interferon cDNA.";

RL Nucleic Acids Res. 18:6724-6724 (1990).

RN [5]

RP SEQUENCE OF 24-195 FROM N.A. (IFN-TAU2A AND IFN-TAU2B).

RC TISSUE=Embryo;

RA Winkelman G.L., Roberts R.M., Peterson A.J., Alexenko A.P., Ealy A.D.;

RT "Identification of the expressed forms of ovine interferon-tau in the peri-implantation conceptus: sequence relationships and comparative biological activities.";

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

RN [6]

RX SEQUENCE OF 24-68.

RX MEDLINE=88137579; PubMed=3254170; DOI=10.1016/0014-5793(88)80574-X;

RA Charigny G., Reinard P., Hue J.-C., Guillemot M., Charlier M., Bernollet J.-C., Marcal J.;

RT "High homology between a trophoblastic protein (trophoblastin) isolated from ovine embryo and alpha-interferons.";

RL FEBS Lett. 228:12-16 (1988).

RN [7]

RP FUNCTION.

RX MEDLINE=96174804; PubMed=8603586; DOI=10.1210/en.137.3.1144;

RA Spencer T.E., Bazer F.W.;

RT "Ovine interferon tau suppresses transcription of the estrogen receptor and oxytocin receptor genes in the ovine endometrium.";

RL Endocrinology 137:1144-1147 (1996).

RL J. Interferon Cytokine Res. 15:1053-1060(1995) .
 RN [5]
 RP REVIEW
 RX MEDLINE=99081096; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
 RA Martal J.L., Chene N.M., Huynh L.P., L'Hardon R.M., Reinard P.B.,
 RA Guillomot M.W., Charpigny M.A., Charpigny S.Y.;
 RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-
 RT ubiquitous expression, structure-function relationships, a pregnancy
 RT hormonal embryonic signal and cross-species therapeutic
 RT potentialities";
 RL Biochimie 80:755-777(1998) .
 CC -1- FUNCTION: Paracrine hormone primarily responsible for maternal
 CC recognition of pregnancy. Interacts with endometrial receptors,
 CC probably type I interferon receptors, and blocks estrogen receptor
 CC expression, preventing the estrogen-induced increase in oxytocin
 CC receptor expression in the endometrium. This results in the
 CC suppression of the pulsatile endometrial release of the luteolytic
 CC hormone prostaglandin F2-alpha, hindering the regression of the
 CC corpus luteum (luteolysis) and therefore a return to ovarian
 CC cyclicity. This, and a possible direct effect of IFN-tau on
 CC prostaglandin synthesis, leads in turn to continued ovarian
 CC progesterone secretion, which stimulates the secretion by the
 CC endometrium of the nutrients required for the growth of the
 CC conceptus. In summary, displays particularly high antiviral and
 CC antiproliferative potency concurrently with particular weak
 CC cytotoxicity, high antiluteolytic activity and immunomodulatory
 CC properties. In contrast with other IFNs, IFN-tau is not vitally
 CC inducible.
 CC -1- SUBCELLULAR LOCATION: Secreted into the uterine lumen.
 CC -1- TISSUE SPECIFICITY: Constitutively and exclusively expressed in
 CC the mononuclear cells of the extra-embryonic trophoblast.
 CC -1- DEVELOPMENTAL STAGE: Major secretory product synthesized by the
 CC sheep conceptus between days 13 and 21 of pregnancy.
 CC -1- POLYMORPHISM: There seems to be two variants of IFN-tau 3: A/88V1
 CC (shown here) and B/P8V3.
 CC -1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from
 CC IFN-omega genes in the ruminantia suborder and have continued to
 CC duplicate independently in different lineages of the ruminantia.
 CC They encode for proteins very similar in sequence but with
 CC different biological potency and pattern of expression.
 CC -1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-
 CC alpha1 subfamily.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.jdb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: AF158817; AAD4969.1; -;
 DR EMBL: AF158819; AAD4971.1; -;
 DR HSSP: P56828; 1BSL.
 DR InterPro: IPR005079; 4_helix_cytokine.
 DR InterPro: IPR000471; Interferon_abd.
 DR Pfam: PF00143; Interferon_1.
 DR PRINTS: PR00266; INTERFERONAB.
 DR PRODOM: PD000550; Interferon_abd.1.
 DR PROSITE: PS00252; INTERFERON_A_B_D; FALSE NEG.
 KW Antiviral; Cytokine; Hormone; Multigene family; Polymorphism;
 KW Pregnancy.
 FT DISULFID 1 99 By similarity.
 FT DISULFID 29 139 T->S (in isoform B).
 FT VARIANT 87 87 FE -> SQ (in isoform B).
 FT VARIANT 124 125 L -> Y (in isoform B).
 FT VARIANT 130 130
 SQ SEQUENCE 172 AA; 19866 MW; 7BPF1F036545C8B2 CRC64;
 Query Match 97.9%; Score 888; DB 1; Length 172;
 Best Local Similarity 97.7%; Pred. No. 1.6e-74;
 Matches 168; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CYLSRKLMDPARENKLLDNRNLSPHSCLODRKDFGLPOBWNVGDQLOKDOAPFLVYEM 60
 Db 1 CYLSERLMDARENKLLDNRNLSPHSCLODRKDFGLPOBWNVGDQLOKDOAFPLVYEM 60
 QY 61 LOOSFNLFYTEHSSAAMDITLLEQLCTGLQOQLDHLDTGCGVWGEEDSELGNDPIVTV 120
 Db 61 LOOSFNLFYTEHSSAAMDITLLEQLCTGLQOQLDHLDTGCGVWGEEDSELGNDPIVTV 120
 QY 121 KXFFGGYDYLQKGYSDCAMEIVRVMRALVSTTLQKRLTKMGSDLNSP 172
 Db 121 KXFFGGYDYLQKGYSDCAMEIVRVMRALVSTTLQKRLTKMGSDLNSP 172
 RESULT 4
 INT4_SHEEP STANDARD; PRT; 195 AA.
 AC Q28594;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interferon tau-4 precursor (IFN-tau4) (Trophoblast protein-1) (TP-1)
 DE (Trophoblastin) (Antiluteolytic) (Trophoblast antiluteolytic protein)
 DE (P3).
 GN Name=IFNT4;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 OC NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=91067497; PubMed=1701245;
 RA Klemann S.W., Imakawa K., Roberts R.M.;
 RT "Sequence variability among ovine trophoblast interferon cDNA";
 RL Nucleic Acids Res. 18:6724-6724(1990).
 RN [2]
 RP FUNCTION.
 RX MEDLINE=96174804; PubMed=8603586; DOI=10.1210/en.137.3.1144;
 RA Spencer T.E., Bazer F.W.;
 RT "Ovine Interferon tau suppresses transcription of the estrogen
 RT receptor and oxytocin receptor genes in the ovine endometrium";
 RL Endocrinology 137:1144-1147(1996).
 RN [3]
 RP CIRCULAR DICHOISM ANALYSIS, AND 3D-STRUCTURE MODELING.
 RX MEDLINE=95062134; PubMed=7971949;
 RA Urpe M.A., Johnson H.M., Bazer F.W., Ott T.L., Curro E.V.,
 RA Krishna N.R., Pontzer C.H.;
 RT "Predicted structural motif of IFN tau";
 RL Protein Eng. 7:863-867(1994).
 RN [4]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=96318252; PubMed=8746786;
 RA Senda T., Saitoh S.-I., Mitsui Y., Li J., Roberts R.M.;
 RT "A three-dimensional model of interferon-tau";
 RL J. Interferon Cytokine Res. 15:1053-1060(1995).
 RN [5]
 RP REVIEW.
 RX MEDLINE=99081096; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
 RA Martal J.L., Chene N.M., Huynh L.P., L'Hardon R.M., Reinard P.B.,
 RA Guillomot M.W., Charpigny M.A., Charpigny S.Y.;
 RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-
 RT ubiquitous expression, structure-function relationships, a pregnancy
 RT hormonal embryonic signal and cross-species therapeutic
 RT potentialities";
 RL Biochimie 80:755-777(1998) .
 CC -1- FUNCTION: Paracrine hormone primarily responsible for maternal
 CC recognition of pregnancy. Interacts with endometrial receptors,
 CC probably type I interferon receptors, and blocks estrogen receptor
 CC expression, preventing the estrogen-induced increase in oxytocin
 CC receptor expression in the endometrium. This results in the
 CC suppression of the pulsatile endometrial release of the luteolytic
 CC hormone prostaglandin F2-alpha, hindering the regression of the

corpus luteum (luteolysis) and therefore a return to ovarian cyclicity. This, and a possible direct effect of IFN-tau on prostaglandin synthesis, leads in turn to continued ovarian progesterone secretion, which stimulates the secretion by the endometrium of the nutrients required for the growth of the conceptus. In summary, displays particularly high antiviral and antiproliferative potency concurrently with particular weak cytotoxicity, high antiluteolytic activity and immunomodulatory properties. In contrast with other IFNs, IFN-tau is not vitally inducible.

-1- SUBCELLULAR LOCATION: Secreted into the uterine lumen.

-1- TISSUE SPECIFICITY: Constitutively and exclusively expressed in the mononuclear cells of the extra-embryonic trophoblast.

-1- DEVELOPMENTAL STAGE: Major secretory product synthesized by the sheep conceptus between days 13 and 21 of pregnancy.

-1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from IFN-omega genes in the ruminantia suborder and have continued to duplicate independently in different lineages of the ruminantia. They encode for proteins very similar in sequence but with different biological potency and pattern of expression.

-1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-alpha1 subfamily.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to license@ebi.ac.uk).

DR EMBL: X56341, CA93781.1; -.

DR HSBP: P56828; 185L.

DR InterPro: IPR009079; 4_helix_cytokine.

DR InterPro: IPR000471, Interferon_abd.

DR Pfam: PF00143; Interferon_1.

DR PRINTS: PR00266; INTERFERONAB.

DR PRODOM: PD000550; Interferon_abd. 1.

DR PROSITE: PS00253; INTERFERON_A_B_D; 1.

DR Antiviral; Cytokine; Hormone; Multigene family; Pregnancy; Signal.

FT SIGNAL 1 23 By similarity.

FT CHAIN 24 195 Interferon tau-4.

FT DISULFID 24 122 By similarity.

FT DISULFID 52 162 By similarity.

SQ SEQUENCE 195 AA; 22209 MW; 408BD4BDF5AA931 CRC64;

Query Match 97.1%; Score 881; DB 1; Length 195;
Best Local Similarity 96.5%; Pred. No. 8.5e-74;
Matches 166; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 CYLSRLMLDARENLKILDRNRLSPHSCLODRKDFGLPQEMVEGDLQKQAPFVLYEM 60
DQ 24 CYLSQRLMLDARENLKILDRNRLSPHSCLODRKDFGLPQEMVEGDLQKQAPFVLYEM 83
QY 61 LQGSFNLFYTHSSAANDTLLDGLCTGLQOOLDLPTCRGQVNGEBSSEIGNNDPIVTY 120
DQ 84 LQGSFNLFYTHSSAANDTLLDGLCTGLQOOLDLPTCRGQVNGEBSSEIGNNDPIVTY 143
QY 121 KKYVQGIYDYLOEKGYSDCAWEIVRVEMRALVTSTLQKRLTKMGGLNSP 172
DQ 144 KKYVQGIYDYLOEKGYSDCAWEIVRVEMRALVTSTLQKRLTKMGGLNSP 195

RESULT 5
INT7 SHEEP
ID INT7 SHEEP STANDARD, PRT; 195 AA.
AC 008071;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interferon tau-7 precursor (IFN-tau7) (Trophoblast protein-1) (TP-1) (Trophoblastin) (Antiluteolytic) (Trophoblast antiluteolytic protein) (TP-07).

GN Name=IFN7;
OS Ovis aries (sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxId=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Trophoblast;
RX MEDLINE=93250155; PubMed=9485241;
RA Nephew K.P., Whaley A.E., Christenson R.K., Imakawa K.;
RT "Differential expression of distinct mRNAs for ovine trophoblast protein-1 and related sheep type I interferons.";
RL Biol. Reprod. 48:768-778(1993).
RN [2]
RP FUNCTION.
RX MEDLINE=96174804; PubMed=8603586; DOI=10.1210/en.137.3.1144;
RA Spencer T.E., Bazer F.W.;
RT "Ovine interferon tau suppresses transcription of the estrogen receptor and oxytocin receptor genes in the ovine endometrium.";
RL Endocrinology 137:1144-1147(1996).
RN [3]
RP CIRCULAR DICHOISM ANALYSIS, AND 3D-STRUCTURE MODELING.
RX MEDLINE=95062134; PubMed=7971949;
RA Jarpe M.A., Johnson H.M., Bazer F.W., Oct T.L., Curto E.V.,
RA Krishna N.R., Pontzer C.H.;
RT "Predicted structural motif of IFN tau.";
RL Protein Eng. 7:863-867(1994).
RN [4]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=96318252; PubMed=8746786;
RA Senda T., Saitoh S.-I., Mitsui Y., Li J., Roberts R.M.;
RT "A three-dimensional model of interferon-tau.";
RL J. Interferon Cytokine Res. 15:1053-1060(1995).
RN [5]
RP REVIEW.
RX MEDLINE=99081096; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
RA Martal J.L., Chene N.M., Huynh L.P., L'Hardon R.M., Reinard P.B.,
RA Guillomot M.W., Charlier M.A., Charpigny S.Y.;
RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-ubiquitous expression, structure-function relationships, a pregnancy hormonal embryonic signal and cross-species therapeutic potentialities.";
RL Biochimie 80:755-777(1998).
CC -1- FUNCTION: Paracrine hormone primarily responsible for maternal recognition of pregnancy. Interacts with endometrial receptors, probably type I interferon receptors, and blocks estrogen receptor expression, preventing the estrogen-induced increase in oxytocin receptor expression in the endometrium. This results in the suppression of the pulsatile endometrial release of the luteolytic hormone prostaglandin F2-alpha, hindering the regression of the corpus luteum (luteolysis) and therefore a return to ovarian cyclicity. This, and a possible direct effect of IFN-tau on prostaglandin synthesis, leads in turn to continued ovarian progesterone secretion, which stimulates the secretion by the endometrium of the nutrients required for the growth of the conceptus. In summary, displays particularly high antiviral and antiproliferative potency concurrently with particular weak cytotoxicity, high antiluteolytic activity and immunomodulatory properties. In contrast with other IFNs, IFN-tau is not vitally inducible.

-1- SUBCELLULAR LOCATION: Secreted into the uterine lumen.

-1- TISSUE SPECIFICITY: Constitutively and exclusively expressed in the mononuclear cells of the extra-embryonic trophoblast.

-1- DEVELOPMENTAL STAGE: Major secretory product synthesized by the sheep conceptus between days 13 and 21 of pregnancy.

-1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from IFN-omega genes in the ruminantia suborder and have continued to duplicate independently in different lineages of the ruminantia. They encode for proteins very similar in sequence but with different biological potency and pattern of expression.

-1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-alpha1 subfamily.

```

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; M88771; AAA31505.1; -.
DR PIR; I47068; I47068.
DR HSSP; P56828; IBSL.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon_1.
DR PRINTS; PR00266; INTERFERONAB.
DR PRODOM; PD000550; Interferon_abd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
DR Antiviral; Cytokine; Hormone; Multigene family; Pregnancy; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 195 Interferon tau-7.
FT DISULFID 24 122 By similarity.
FT DISULFID 52 162 By similarity.
SQ SEQUENCE 195 AA; 22223 MW; 144ADE80AAB48 CRC64;

Query Match 97.0%; Score 880; DB 1; Length 195;
Best Local Similarity 96.5%; Pred. No. 1.1e-73;
Matches 166; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CYLSRKLMLDARENLKLLDRNRSLPSHSCLODRKDFGLPQEMVEGDLQKQDAFVLYEM 60
DB 24 CYSRRRLMLDARENLRLDRNRSLPSHSCLODRKDFGLPQEMVEGDLQKQDAFVLYEM 83
QY 61 LQSFNLFYTHSSAAMDITLLEQLCTGLQQLDPLPCRGQVNGEBSLGNMDPIVTV 120
DB 84 LQSFNLFYTHSSAAMDITLLEQLCTGLQQLDPLPCRGQVNGEBSLGNMDPIVTV 143
QY 121 KKVFQGIYDYLOEKGYSDCAEIVREVMRALTVSTTLQKRLTGMGDLNSP 172
DB 144 KKVFQGIYDYLOEKGYSDCAEIVREVMRALTVSTTLQKRLTGMGDLNSP 195

RESULT 6
INTS SHEEP STANDARD; PRT; 195 AA.
ID INTS SHEEP STANDARD; PRT; 195 AA.
AC 028595;
AD 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interferon tau-5 precursor (IFN-taus) (Trophoblast protein-1)
DE (Trophoblastin) (Antiluteolysin) (Trophoblast antiluteolytic protein)
DE (F5).
GN Name=IFNT5;
OS Ovis aries (sheep).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metazoa; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91067497; PubMed=1701245;
RA Klemann S.W., Inakawa K., Roberts R.M.;
RT "Sequence variability among ovine trophoblast interferon cDNA.";
RL Nucleic Acids Res. 18:6724-6724(1990).
RN [2]
RP FUNCTION.
RX MEDLINE=96174804; PubMed=8603586; DOI=10.1210/en.137.3.1144;
RA Spencer T.E., Bazer F.W.;
RT "Ovine interferon tau suppresses transcription of the estrogen
RT receptor and oxytocin receptor genes in the ovine endometrium.";
RL Endocrinology 137:1144-1147(1996).
RN [3]
RP CIRCULAR DICHOISM ANALYSIS, AND 3D-STRUCTURE MODELING.

```

```

RX MEDLINE=95062134; PubMed=7971949;
RA Jarpe M.A., Johnson H.M., Bazer F.W., Ott T.L., Curro E.V.,
RA Krishna N.R., Pontzer C.H.;
RT "Predicted structural motif of IFN tau.";
RL Protein Eng. 7:863-867(1994).
RN [4]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=96318252; PubMed=8746786;
RA Senda T., Saitoh S.-I., Mitsui Y., Li J., Roberts R.M.;
RT "A three-dimensional model of interferon-tau.";
RL J. Interferon Cytokine Res. 15:1053-1060(1995).
RN [5]
RP REVIEW.
RX MEDLINE=99081096; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
RA Martal J.L., Chene N.M., Huynh L.P., L'Hardion R.M., Reinard P.B.,
RA Guillouet M.W., Charlier M.A., Chapigny S.Y.;
RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-
RT ubiquitous expression, structure-function relationships, a pregnancy
RT hormonal embryonic signal and cross-species therapeutic
RT potentialities.";
RL Biochimie 80:755-777(1998).
CC -1- FUNCTION: Paracrine hormone primarily responsible for maternal
CC recognition of pregnancy. Interacts with endometrial receptors,
CC probably type I interferon receptors, and blocks estrogen receptor
CC expression, preventing the estrogen-induced increase in oxytocin
CC receptor expression in the endometrium. This results in the
CC suppression of the pulsatile endometrial release of the luteolytic
CC hormone prostaglandin F2-alpha, hindering the regression of the
CC corpus luteum (luteolysis) and therefore a return to ovarian
CC cyclicity. This, and a possible direct effect of IFN-tau on
CC prostaglandin synthesis, leads in turn to continued ovarian
CC progesterone secretion, which stimulates the secretion by the
CC endometrium of the nutrients required for the growth of the
CC conceptus. In summary, displays particularly high antiviral and
CC antiproliferative potency concurrently with particular weak
CC cytotoxicity, high antiluteolytic activity and immunomodulatory
CC properties. In contrast with other IFNs, IFN-tau is not vitally
CC inducible.
CC -1- SUBCELLULAR LOCATION: Secreted into the uterine lumen.
CC -1- TISSUE SPECIFICITY: Constitutively and exclusively expressed in
CC the mononuclear cells of the extra-embryonic trophoblast.
CC -1- DEVELOPMENTAL STAGE: Major secretory product synthesized by the
CC sheep conceptus between days 13 and 21 of pregnancy.
CC -1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from
CC IFN-omega genes in the ruminantia suborder and have continued to
CC duplicate independently in different lineages of the ruminantia.
CC They encode for proteins very similar in sequence but with
CC different biological potency and pattern of expression.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-
CC alpha1 subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; X56342; CAJ3782.1; -.
DR HSSP; P56828; IBSL.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon_1.
DR PRINTS; PR00266; INTERFERONAB.
DR PRODOM; PD000550; Interferon_abd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
DR Antiviral; Cytokine; Hormone; Multigene family; Pregnancy; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 195 Interferon tau-5.
FT DISULFID 24 122 By similarity.
FT DISULFID 52 162 By similarity.
SQ SEQUENCE 195 AA; 22163 MW; 14EA9038CB60A562 CRC64;

```


AC Q08072;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Interferon tau-8 precursor (IFN-tau8) (Trophoblast protein-1) (TP-1)
 DE (Trophoblastin) (Antiluteolysin) (Trophoblast antiluteolytic protein)
 DE (TP-08).
 GN Name=IFNT8;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 OC NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TTSUB=Tyrocytoderma;
 RA MEDLINE=93250155; PubMed=8485241;
 RA Nephew K.P., Whaley A.E., Christenson R.K., Imakawa K.;
 RT "Differential expression of distinct mRNAs for ovine trophoblast
 RT protein-1 and related sheep type I interferons.";
 RL Biol. Reprod. 46:768-778(1993).
 RN [2]
 RP FUNCTION.
 RA MEDLINE=96174804; PubMed=8603586; DOI=10.1210/en.137.3.1144;
 RA Spencer T.E., Bazer F.W.;
 RT "Ovine interferon tau suppresses transcription of the estrogen
 RT receptor and oxytocin receptor genes in the ovine endometrium.";
 RL Endocrinology 137:1144-1147(1996).
 RN [3]
 RP CIRCULAR DICHOISM ANALYSIS, AND 3D-STRUCTURE MODELING.
 RA MEDLINE=95062134; PubMed=7971949;
 RA Jarpe M.A., Johnson H.M., Bazer F.W., Ott T.L., Curto E.V.,
 RA Krishna N.R., Pontzer C.H.;
 RT "Predicted structural motif of IFN tau.";
 RL Protein Eng. 7:863-867(1994).
 RN [4]
 RP 3D-STRUCTURE MODELING.
 RA MEDLINE=96318252; PubMed=8746786;
 RA Senda T., Saitoh S.-I., Mitani Y., Li J., Roberts R.M.;
 RT "A three-dimensional model of interferon-tau.";
 RL J. Interferon Cytokine Res. 15:1053-1060(1995).
 RN [5]
 RP REVIEW.
 RA MEDLINE=99081096; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
 RA Matall J.L., Chene N.M., Huynh L.P., L'Hardion R.M., Reinard P.B.;
 RA Galloway M.W., Charlier M.A., Charigny S.Y.;
 RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-
 RT ubiquitous expression, structure-function relationships, a pregnancy
 RT hormonal embryonic signal and cross-species therapeutic
 RT potentialities.";
 RL Biochimie 80:755-777(1998).
 CC -1- FUNCTION: Paracrine hormone primarily responsible for maternal
 CC recognition of pregnancy. Interacts with endometrial receptors,
 CC probably type I interferon receptors, and blocks estrogen receptor
 CC expression, preventing the estrogen-induced increase in oxytocin
 CC receptor expression in the endometrium. This results in the
 CC suppression of the pulsatile endometrial release of the luteolytic
 CC hormone prostaglandin F2-alpha, hindering the regression of the
 CC corpus luteum (luteolysis) and therefore a return to ovarian
 CC cyclicity. This, and a possible direct effect of IFN-tau on
 CC prostaglandin synthesis, leads in turn to continued ovarian
 CC progesterone secretion, which stimulates the secretion by the
 CC endometrium of the nutrients required for the growth of the
 CC conceptus. In summary, displays particularly high antiviral and
 CC antiproliferative potency concurrently with particular weak
 CC cytotoxicity, high antiluteolytic activity and immunomodulatory
 CC properties. In contrast with other IFNs, IFN-tau is not virally
 CC inducible.
 CC -1- SUBCELLULAR LOCATION: Secreted into the uterine lumen.
 CC -1- TISSUE SPECIFICITY: Constitutively and exclusively expressed in
 CC the mononuclear cells of the extra-embryonic trophoderm.
 CC -1- DEVELOPMENTAL STAGE: Major secretory product synthesized by the
 CC sheep conceptus between days 13 and 21 of pregnancy.

CC -1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from
 CC IFN-omega genes in the ruminantia suborder and have continued to
 CC duplicate independently in different lineages of the ruminantia.
 CC They encode for proteins very similar in sequence but with
 CC different biological potency and pattern of expression.
 CC -1- SIMILARITY: Belongs to the alpha/beta interferon family, IFN-
 CC alpha1 subfamily.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL: M88772; AAA31506.1; -;
 CC PIR: I47069; I47069.
 CC DR HSP: P56828; IBSL.
 CC DR InterPro: IPR009079; 4 helix cytokine.
 CC DR InterPro: IPR000471; Interferon_abd.
 CC DR Pfam: PF00143; Interferon_1.
 CC DR PRINTS: PR00266; INTERFERONAB.
 CC DR PRODOM: PD000550; Interferon_abd_1.
 CC DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
 CC KM Activiral; Cytokine; Hormone; Multigene family; Pregnancy; Signal.
 CC FT SIGNAL 1 23 By similarity.
 CC FT CHAIN 24 195 Interferon tau-8.
 CC FT DISULFID 24 122 By similarity.
 CC FT DISULFID 52 162 By similarity.
 CC SQ SEQUENCE 195 AA; 22157 MW; 7F92C56EC8DB5A8 CRC64;
 CC -----
 CC Query Match 95.4%; Score 865; DB 1; Length 195;
 CC Best Local Similarity 94.8%; Pred. No. 2.6e-72;
 CC Matches 163; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 CC -----
 CC QY 1 CYLSRKLMDARENLKLDNRNRLSPHSCQDRKDFGLPQEMVGGDLOKDOAFVLYEM 60
 CC Db 24 CYLSQRLMDARENLRLDMNRNLSPHSCQDRKDFGLPQEMVGGDLOKDOAFVLYEM 83
 CC QY 61 LQGSFNLFTYHSSAAMDITLLBOLCTGLQOQLDHLDTGCGQVGEEDSELGNMPPVTV 120
 CC Db 84 LQGSFNLFTYHSSAAMDITLLDOLCTGLQOQLEDLDTGCGVGEEDSELGNMPPVTV 143
 CC QY 121 KKFQGGYDYLQKGYSDCAWEIVRVMRALTVSTTLQKRLFTGMGDLNSP 172
 CC Db 144 KKFQGGYDYLQKGYSDCAWEIVRVMRALTVSTTLQKRLFTGMGDLNSP 195
 CC -----
 CC RESULT 9
 CC INT_CAPIH
 CC ID_INT_CAPIH STANDARD; PRT; 195 AA.
 CC AC P28171;
 CC DT 30-MAY-2000 (Rel. 39, Created)
 CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
 CC DT 05-JUN-2004 (Rel. 44, Last annotation update)
 CC DE Interferon tau precursor (IFN-tau) (Trophoblast protein-1) (TP-1)
 CC DE (Trophoblastin) (Antiluteolysin) (Trophoblast antiluteolytic protein).
 CC GN Name=IFNT; Synonyms=CIP-1;
 CC OS Capra hircus (Goat).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC OC Caprinae; Capra.
 CC OC NCBI_TaxID=9925;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RA MEDLINE=92242937; PubMed=1374107;
 CC RA Leaman D.W., Roberts R.M.;
 CC RT "Genes for the trophoblast interferons in sheep, goat, and musk ox and
 CC RT distribution of related genes among mammals.";
 CC RL J. Interferon Res. 12:1-11(1992).
 CC RN [2]
 CC REVIEW.

RX MEDLINE=99081096; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
 RA Matral J.L., Chene N.M., Huynh L.P., L'Hartidon R.M., Reinaud P.B.,
 RA Guillomot M.W., Charlier M.A., Charpigny S.Y.;
 RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-
 RT ubiquitous expression, structure-function relationships, a pregnancy
 RT hormonal embryonic signal and cross-species therapeutic
 RT potentialities".
 RT Blochimie 80:755-777(1998).
 RL -1- FUNCTION: Paracrine hormone primarily responsible for maternal
 CC recognition of pregnancy. Interacts with endometrial receptors,
 CC probably type I interferon receptors, and blocks estrogen receptor
 CC expression, preventing the estrogen-induced increase in oxytocin
 CC receptor expression in the endometrium. This results in the
 CC suppression of the pulsatile endometrial release of the luteolytic
 CC hormone progesterone in P2-alpha, hindering the regression of the
 CC corpus luteum (luteolysis) and therefore a return to ovarian
 CC cyclicity. This, and a possible direct effect of IFN-tau on
 CC progesterone synthesis, leads in turn to continued ovarian
 CC progesterone secretion, which stimulates the secretion by the
 CC endometrium of the nutrients required for the growth of the
 CC conceptus. In summary, displays particularly high antiviral and
 CC antiproliferative potency concurrently with particular weak
 CC cytotoxicity, high antiluteolytic activity and immunomodulatory
 CC properties. In contrast with other IFNs, IFN-tau is not vitally
 CC inducible.
 CC -1- SUBCELLULAR LOCATION: Secreted into the uterine lumen.
 CC -1- TISSUE SPECIFICITY: Constitutively and exclusively expressed in
 CC the mononuclear cells of the extra-embryonic trophoblast.
 CC -1- DEVELOPMENTAL STAGE: Major secretory product synthesized by the
 CC conceptus during a very short period in early pregnancy.
 CC -1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from
 CC IFN-omega genes in the ruminant suborder and have continued to
 CC duplicate independently in different lineages of the ruminantia.
 CC They encode for proteins very similar in sequence but with
 CC different biological potency and pattern of expression.
 CC -1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-
 CC alpha1 subfamily.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL/ M73243; AAA30907.1; -;
 DR PIR/ I46272; I46272.
 DR HSRP/ P56828; I85L.
 DR InterPro/ IPR009079; 4_helix_cytokine.
 DR InterPro/ IPR000471; Interferon_abd.
 DR Pfam/ PF00143; Interferon_1.
 DR PRINTS/ PR00266; INTERFERONAB.
 DR ProDom/ PD000550; Interferon abd. 1.
 DR PROSITE/ PS00252; INTERFERON_A_B_D_1.
 KM Antiviral; Cytokine; Hormone; Pregnancy; Signal.
 FT SIGNAL 1 23 By similarity.
 FT CHAIN 24 195 Interferon tau.
 FT DISULFID 24 122 By similarity.
 FT DISULFID 52 162 By similarity.
 SQ SEQUENCE 195 AA; 22172 MW; 049F91D3EB1CDB67 CRC64;
 Query Match 93.3%; Score 846; DB 1; Length 195;
 Best Local Similarity 93.6%; Pred. No. 1.5e-70;
 Matches 161; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 121 KKYFQGIYDIYOEKGYSDCAWEIVEMRALTIVSTLQKRLTMGGDLSNP 172
 DB 144 KKYFQGIYDIYOEKGYSDCAWEIVEMRALTIVSTLQKRLTMGGDLSNP 195
 RESULT 10
 ID INT6 SHEEP STANDARD; PRT; 195 AA.
 AC Q29429;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Interferon tau-6 precursor (IFN-tau6) (Trophoblast protein-1) (TP-1)
 DE (Trophoblastin) (Antiluteolytic) (Trophoblast antiluteolytic protein).
 GN Name=IFN6;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A. (IFN-TAU6D).
 RC TISSUE=Embryo;
 RX MEDLINE=91067497; PubMed=1701245;
 RA Klemann S.W., Imakawa K., Roberts R.M.;
 RT "Sequence variability among ovine trophoblast interferon cDNA.";
 RL Nucleic Acids Res. 18:6724-6724(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (IFN-TAU6D).
 RA Roberts R.M.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 24-195 FROM N.A. (IFN-TAU6A; IFN-TAU6B AND IFN-TAU6C).
 RC TISSUE=Embryo;
 RA Winkelman G.L., Roberts R.M., Peterson A.J., Alexenko A.P., Ealy A.D.;
 RT "Identification of the expressed forms of ovine interferon-tau in the
 RT peri-implantation conceptus: sequence relationships and comparative
 RT biological activities.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP FUNCTION.
 RX MEDLINE=96174804; PubMed=8603586; DOI=10.1210/en.137.3.1144;
 RA Spencer T.E., Bazer F.W.;
 RT "Ovine interferon tau suppresses transcription of the estrogen
 RT receptor and oxytocin receptor genes in the ovine endometrium.";
 RL Endocrinology 137:1144-1147(1996).
 RN [5]
 RP CIRCULAR DICHOISM ANALYSIS, AND 3D-STRUCTURE MODELING.
 RX MEDLINE=95062134; PubMed=7971949;
 RA Jarpe M.A., Johnson H.M., Bazer F.W., Ott T.L., Curto E.V.,
 RA Krishna N.R., Pontzer C.H.;
 RT "Predicted structural motif of IFN tau.";
 RL Protein Eng. 7:863-867(1994).
 RN [6]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=96318252; PubMed=8746786;
 RA Senda T., Saitoh S.-I., Mitsui Y., Li J., Roberts R.M.;
 RT "A three-dimensional model of interferon-tau.";
 RL J. Interferon Cytokine Res. 15:1053-1060(1995).
 RN [7]
 RP REVIEW.
 RX MEDLINE=99081096; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
 RA Matral J.L., Chene N.M., Huynh L.P., L'Hartidon R.M., Reinaud P.B.,
 RA Guillomot M.W., Charlier M.A., Charpigny S.Y.;
 RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-
 RT ubiquitous expression, structure-function relationships, a pregnancy
 RT hormonal embryonic signal and cross-species therapeutic
 RT potentialities".
 RL Blochimie 80:755-777(1998).
 CC -1- FUNCTION: Paracrine hormone primarily responsible for maternal
 CC recognition of pregnancy. Interacts with endometrial receptors,
 CC probably type I interferon receptors, and blocks estrogen receptor

RA Ealy A.D., Wagner S.K., Shells A.E., Whitley N.C., Klesling D.O.,
RA Barbaco G.F.,
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
DR EMBL: AY357328; AAC6197.1; -.
DR EMBL: AY357327; AAC6196.1; -.
DR HSSP: P56828; 1BSL.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005126; F:hematopoietin/interferon-classes (D200-domain. . .); IEA.
DR GO: GO:0006952; P:defense response; IEA.
DR InterPro: IPR009079; 4_helix_cytokine.
DR InterPro: IPR00471; Interferon_abd.
DR Pfam: PF00143; Interferon; 1.
DR PRINTS: PR00266; INTERFERONAB.
DR ProDom: PD000550; Interferon_abd; 1.
DR SMART: SM00076; IFabd; 1.
DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine.
SQ SEQUENCE 195 AA; 22313 MW; C99AC236A716F654 CRC64;

Query March 91.5%; Score 830; DB 2; Length 195;
Best Local Similarity 92.4%; Pred. No. 4.7e-69;
Matches 159; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENILKILDRNRRLSPHSCLODRKDFGLPQEMVEGDLQKQDAFPVLYEM 60
DB 24 CYLSRRMLDARENILKILDRNRRLSPHSCLODRKDFGLPQEMVEGDLQKQDAFSLVLYEM 83
QY 61 LQGSFNLFTYTHSSAAMDITLLLEQLCTGLQOOLDLHLDTCRGQVNGEEDSEIGNMDPIVTV 120
DB 84 LQGFNLFYTHSSAAMDITLLLEQLCTGLQOOLDLHLDTCRGQVNGEEDSEIGNMDPIVTV 143
QY 121 KKYFGIYDYLQEKYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 172
DB 144 KKYFGIYDYLQEKYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 195

RESULT 13
Q6RFZ8 PRELIMINARY; PRT; 172 AA.
AC Q6RFZ8
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Interferon tau (fragment).
OS Ovis aries (sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
NCBI_TaxID=9940;
RN NCB1
RP SEQUENCE FROM N.A.
RA Wang X., Wang M., Xia C., Zhu D., Liou C., Bai Y.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
DR EMBL: AY49657; AAR5892.1; -.
DR HSSP: P56828; 1BSL.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005126; F:hematopoietin/interferon-classes (D200-domain. . .); IEA.
DR GO: GO:0006952; P:defense response; IEA.
DR InterPro: IPR009079; 4_helix_cytokine.
DR InterPro: IPR00471; Interferon_abd.
DR Pfam: PF00143; Interferon; 1.
DR PRINTS: PR00266; INTERFERONAB.
DR ProDom: PD000550; Interferon_abd; 1.
DR SMART: SM00076; IFabd; 1.
DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine.
FT NON_TER 1
SQ SEQUENCE 172 AA; 19992 MW; 65984B2F91335046 CRC64;

Query March 90.0%; Score 816; DB 2; Length 172;
Best Local Similarity 91.3%; Pred. No. 8e-68;

Matches 157; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENILKILDRNRRLSPHSCLODRKDFGLPQEMVEGDLQKQDAFPVLYEM 60
DB 1 CYLSRRMLDARENILKILDRNRRLSPHSCLODRKDFGLPQEMVEGDLQKQDAFSLVLYEM 60
QY 61 LQGSFNLFTYTHSSAAMDITLLLEQLCTGLQOOLDLHLDTCRGQVNGEEDSEIGNMDPIVTV 120
DB 61 LQGFNLFYTHSSAAMDITLLLEQLCTGLQOOLDLHLDTCRGQVNGEEDSEIGNMDPIVTV 120
QY 121 KKYFGIYDYLQEKYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 172
DB 121 KKYFGIYDYLQEKYSDCAMEIVREVMRALTVSTTLQKRLTKMGDLNSP 172

RESULT 14
INTA SHEEP STANDARD; PRT; 195 AA.
AC Q08053;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interferon tau-10 precursor (IFN-tau10) (Trophoblast protein-1) (TP-1)
DE (Trophoblastin) (Antiluteolysin) (Trophoblast antiluteolytic protein)
DE (TP-02).
GN Name=IFNT10;
OS Ovis aries (sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
NCBI_TaxID=9940;
RN NCB1
RP SEQUENCE FROM N.A.
RA TISSUE=Trophectoderm;
RC MEDLINE=93250155; PubMed=8485241;
RA Nephew K.P., Whaley A.E., Christenson R.K., Imakawa K.;
RT "Differential expression of distinct mRNAs for ovine trophoblast
RT protein-1 and related sheep type I interferons.";
RL Biol. Reprod. 48:768-778(1993).
RN [2]
RP FUNCTION.
RX MEDLINE=96174804; PubMed=8603586; DOI=10.1210/en.137.3.1144;
RA Spencer T.E., Bazer F.W.;
RT "Ovine interferon tau suppresses transcription of the estrogen
RT receptor and oxytocin receptor genes in the ovine endometrium.";
RL Endocrinology 137:1144-1147(1996).
RN [3]
RP CIRCULAR DICHOISM ANALYSIS, AND 3D-STRUCTURE MODELING.
RX MEDLINE=95062134; PubMed=7971949;
RA Jarpe M.A., Johnson H.M., Bazer F.W., Oct T.L., Curto E.V.,
RA Krishna N.R., Pontzer C.H.;
RT "Predicted structural motif of IFN tau.";
RL Protein Eng. 7:863-867(1994).
RN [4]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=96319252; PubMed=8746786;
RA Senda T., Saitoh S.-I., Mitsui Y., Li J., Roberts R.M.;
RT "A three-dimensional model of interferon-tau.";
RL J. Interferon Cytokine Res. 15:1053-1060(1995).
RN [5]
RP REVIEW.
RX MEDLINE=99081096; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
RA Martal J.L., Chene N.M., Huynh L.P., L'Haxidon R.M., Reinard P.B.,
RA Guillomot M.W., Charlier M., Charpigny S.Y.;
RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-
RT ubiquitous expression, structure-function relationships, a pregnancy
RT hormonal embryonic signal and cross-species therapeutic
RT potentialities.";
RL Biochimie 80:755-777(1998).
CC -1- FUNCTION: Paracrine hormone primarily responsible for maternal
CC recognition of pregnancy. Interacts with endometrial receptors,
CC probably type I interferon receptors, and blocks estrogen receptor
CC expression, preventing the estrogen-induced increase in oxytocin


```

CC receptor expression in the endometrium. This results in the
CC suppression of the pulsatile endometrial release of the luteolytic
CC hormone prostaglandin F2-alpha, hindering the regression of the
CC corpus luteum (luteolysis) and therefore a return to ovarian
CC cyclicity. This, and a possible direct effect of IFN-tau on
CC prostaglandin synthesis, leads in turn to continued ovarian
CC progesterone secretion, which stimulates the secretion by the
CC endometrium of the nutrients required for the growth of the
CC conceptus. In summary, displays particularly high antiviral and
CC antiproliferative potency concurrently with particular weak
CC cytotoxicity, high antiluteolytic activity and immunomodulatory
CC properties. In contrast with other IFNs, IFN-tau is not vitally
CC inducible.
CC
CC -1- SUBCELLULAR LOCATION: Secreted into the uterine lumen.
CC -1- SUBSITE SPECIFICITY: Constitutively and exclusively expressed in
CC the mononuclear cells of the extra-embryonic trophoblast.
CC -1- DEVELOPMENTAL STAGE: Major secretory product synthesized by the
CC sheep conceptus between days 13 and 21 of pregnancy.
CC -1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from
CC IFN-omega genes in the ruminantia suborder and have continued to
CC duplicate independently in different lineages of the ruminantia.
CC They encode for proteins very similar in sequence but with
CC different biological potency and pattern of expression.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-
CC alpha1 subfamily.
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk).
CC -----
CC
CC EMBL; M88770; AAA31504.1; -.
CC F1R; 147067; 147067.
CC HSP; P56828; 1B5L.
CC InterPro: IPR009079; 4 helix cytokine.
CC InterPro: IPR000471; Interferon_abd.
CC Pfam: PF00143; Interferon_1.
CC PRINTS; PR00266; INTERFERONAB.
CC ProDom; PD000550; Interferon_abd; 1.
CC PROSITE; PS00252; INTERFERON_A_B_D; 1.
CC K1M Activator; Cytokine; Glycoprotein; Hormone; Multigene family;
CC K1M Pregnancy; Signal.
CC FT SIGNAL 1 23 By similarity.
CC FT CHAIN 24 195 Interferon tau-10.
CC FT DISULFID 24 122 By similarity.
CC FT DISULFID 52 162 By similarity.
CC FT CARBOHYD 101 101 N-linked (GlcNAc...) (Potential).
CC SO SEQUENCE 195 AA; 22069 MW; 16084C3184AC3963 CRC64;

```

```

Query Match 88.9%; Score 806; DB 1; Length 195;
Best Local Similarity 89.5%; Pred. No. 7.9e-67;
Matches 154; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

```

```

QY 1 CYLSRKMLDARENLKLLDMNRSLSPSCLODRKDFGLPEWVGDLQLOKQAFVLYEM 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 24 CYLSQRMLDARENLKLLDMNRSLSPSCLODRKDFGLPEWVGDLQLOKQAFVLYEM 83
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 LQGSFNLFTYEHSSAAMDITLLBOLCTGLQOQLDHLDTGCGQVGEEDSEISGNDDPIVTY 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 84 LQGSFNLFTYEHSSAAMDITLLBOLCTGLQOQLDHLDTGCGQVGEEDSEISGNDDPIVTY 143
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 KKYFQGIYDYLQEGYSDCAMEIVRVEMRALTSTTLQRLTKMGDGLNSP 172
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 144 KKYFQGIYDYLQEGYSDCAMEIVRVEMRALTSTTLQRLTKMGDGLNSP 195
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

```

RESULT 15
Q6UZ47 PRELIMINARY; PRT; 195 AA.
ID Q6UZ47
AC Q6UZ47;

```

```

DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Interferon-tau 4b (Interferon-tau 4c) (Interferon-tau 4d) (Interferon-
DE tau 4e) (Interferon-tau 4a).
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA Ealy A.D., Wagner S.K., Shells A.E., Whitley N.C., Kneeling D.O.,
RA Barbato G.F.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
DR EMBL; AY357331; AAQ56200.1; -.
DR EMBL; AY357332; AAQ56201.1; -.
DR EMBL; AY357333; AAQ56202.1; -.
DR EMBL; AY357334; AAQ56203.1; -.
DR EMBL; AY357330; AAQ56199.1; -.
DR HSP; P56828; 1B5L.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .); IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR InterPro: IPR009079; 4 helix cytokine.
DR InterPro: IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon_1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IPab; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
DR Activator; Cytokine.
SQ SEQUENCE 195 AA; 22354 MW; D364AC9A972D8FC4 CRC64;

```

```

Query Match 88.6%; Score 804; DB 2; Length 195;
Best Local Similarity 90.1%; Pred. No. 1.2e-66;
Matches 155; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

```

```

QY 1 CYLSRKMLDARENLKLLDMNRSLSPSCLODRKDFGLPEWVGDLQLOKQAFVLYEM 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 24 CYLSRRMLDARENLKLLDMNRSLSPSCLODRKDFGLPEWVGDLQLOKQAFVLYEM 83
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 LQGSFNLFTYEHSSAAMDITLLBOLCTGLQOQLDHLDTGCGQVGEEDSEISGNDDPIVTY 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 84 LQGSFNLFTYEHSSAAMDITLLBOLCTGLQOQLDHLDTGCGQVGEEDSEISGNDDPIVTY 143
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 KKYFQGIYDYLQEGYSDCAMEIVRVEMRALTSTTLQRLTKMGDGLNSP 172
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 144 KKYFQGIYDYLQEGYSDCAMEIVRVEMRALTSTTLQRLTKMGDGLNSP 195
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

```

RESULT 16
Q6UZ43 PRELIMINARY; PRT; 195 AA.
ID Q6UZ43
AC Q6UZ43;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Interferon-tau 5.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA Ealy A.D., Wagner S.K., Shells A.E., Whitley N.C., Kneeling D.O.,
RA Barbato G.F.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
DR EMBL; AY357335; AAQ56204.1; -.
DR HSP; P56828; 1B5L.

```

```

DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005126; P:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO: GO:0006952; P:defense response; IEA.
DR Interferon; IPR009079; 4_helix_cytokine.
DR Interferon; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon_1.
DR PRINTS; PR00266; INTERFERONAB.
DR Prodom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR Antiviral; Cytokine.
SQ SEQUENCE 195 AA; 2236 MW; D37E646A8DE57FC4 CRC64;

Query Match 87.5%; Score 794; DB 2; Length 195;
Best Local Similarity 89.0%; Pred. No. 1e-65;
Matches 153; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

Qy 1 CYLSRKMLDARENLKLLDRNNRLSPHSCLODRKDFGLPQEMVEGDQLQKQAFVLYEM 60
Db 24 CYLSRRMLDARENLRLDRNNRLSPHSCLODRKDFGLPQEMVEGDQLQKQAFVLYEM 83

Qy 61 LQGSFNLFTYEHSSAANDTLLLEQLCTGLOQLDLDTCRGVNGEEDSELGNNDPIVTY 120
Db 84 LQGTFFNLFTYEHSSAANNNTLLLEQLHTGLOQLLEDLTCRGLVNGEKDSELGNNDPIVTY 143

Qy 121 KKYFQGIYDYLQEKGYSDCAMEIVRVMRALTSTTLQKRLTKMGDLNSP 172
Db 144 KRYFQGIHDYLOEKEXYSDCAMEIVRVMRALTSTTLQKRLTKMGDLNSP 195

RESULT 17
06U242 PRELIMINARY; PRT; 195 AA.
AC 06U242;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Interferon-tau 6.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Capra.
OC NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA Ealy A.D., Wagner S.K., Shells A.E., Whitley N.C., Klesling D.O.,
RA Barbato G.F.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
DR EMBL; AY575336; AA056205.1; -.
DR HSSP; P56828; 195L.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005126; P:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO: GO:0006952; P:defense response; IEA.
DR Interferon; IPR009079; 4_helix_cytokine.
DR Interferon; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon_1.
DR PRINTS; PR00266; INTERFERONAB.
DR Prodom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
DR Antiviral; Cytokine.
SQ SEQUENCE 195 AA; 2236 MW; FEE9F24431D41486 CRC64;

Query Match 86.7%; Score 786; DB 2; Length 195;
Best Local Similarity 89.0%; Pred. No. 5.7e-65;
Matches 153; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Qy 1 CYLSRKMLDARENLKLLDRNNRLSPHSCLODRKDFGLPQEMVEGDQLQKQAFVLYEM 60
Db 24 CYLSRRMLDARENLRLDRNNRLSPHSCLODRKDFGLPQEMVEGDQLQKQAFVLYEM 83

Qy 61 LQGSFNLFTYEHSSAANDTLLLEQLCTGLOQLDLDTCRGVNGEEDSELGNNDPIVTY 120

```

```

Db 84 LQGTFFNLFTYEHSSAANNNTLLLEQLHTGLOQLLEDLTCRGLVNGEKDSELGNNDPIVTY 143

Qy 121 KKYFQGIYDYLQEKGYSDCAMEIVRVMRALTSTTLQKRLTKMGDLNSP 172
Db 144 KRYFQGIHDYLOEKEXYSDCAMEIVRVMRALTSTTLQKRLTKMGDLNSP 195

RESULT 18
INT_OVIMO STANDARD; PRT; 195 AA.
AC P28172;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interferon tau precursor (IFN-tau) (Trophoblast protein-1) (TP-1)
DE (Trophoblastin) (Antiluteolytic) (Trophoblast antiluteolytic protein).
GN Name=IFNT; Synonyms=IFN;
OS Ovis bos mesochatus (Muskox).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OC NCBI_TaxID=31176;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92242937; PubMed=1374107;
RA Leaman D.W., Roberts R.M.;
RT "Genes for the trophoblast interferons in sheep, goat, and musk ox and
RT distribution of related genes among mammals."
RL J. Interferon Res. 12:1-11(1992).
RN [2]
RP REVIEW
RX MEDLINE=99081096; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
RA Martal J.L., Chene N.M., Huynh L.P., L'Hardion R.M., Renaud P.B.,
RA Guillomot M.W., Charlier M.A., Charpigny S.Y.;
RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-
RT ubiquitous expression, structure-function relationships, a pregnancy
RT hormonal embryonic signal and cross-species therapeutic
RT potentialities."
RL Biochimie 80:755-777(1998).
CC -1- FUNCTION: Paracrine hormone primarily responsible for maternal
CC recognition of pregnancy. Interacts with endometrial receptors,
CC probably type I interferon receptors, and blocks estrogen receptor
CC expression, preventing the estrogen-induced increase in oxytocin
CC receptor expression in the endometrium. This results in the
CC suppression of the pulsatile endometrial release of the luteolytic
CC hormone prostaglandin F2-alpha, hindering the regression of the
CC corpus luteum (luteolysis) and therefore a return to ovarian
CC cyclicity. This, and a possible direct effect of IFN-tau on
CC prostaglandin synthesis, leads in turn to continued ovarian
CC progesterone secretion, which stimulates the secretion by the
CC endometrium of the nutrients required for the growth of the
CC conceptus. In summary, displays particularly high antiviral and
CC antiproliferative potency concurrently with particular weak
CC cytotoxicity, high antiluteolytic activity and immunomodulatory
CC properties. In contrast with other IFNs, IFN-tau is not virally
CC inducible.
CC -1- SUBCELLULAR LOCATION: Secreted into the uterine lumen.
CC -1- TISSUE SPECIFICITY: Constitutively and exclusively expressed in
CC the mononuclear cells of the extra-embryonic trophoctoderm.
CC -1- DEVELOPMENTAL STAGE: Major secretory product synthesized by the
CC conceptus during a very short period in early pregnancy.
CC -1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from
CC IFN-omega genes in the ruminantia suborder and have continued to
CC duplicate independently in different lineages of the ruminantia.
CC They encode for proteins very similar in sequence but with
CC different biological potency and pattern of expression.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-
CC alpha1 subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

```

CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sb-sib.ch).
 CC -----
 DR EMBL; M73244; AAA31583.1; -.
 DR HSSP; P56828; 185L.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR000471; Interferon_abd.
 DR Pfam; PF00143; Interferon; 1.
 DR PRINTS; PR00266; INTERFERONAB.
 DR ProDom; PD000550; Interferon_abd; 1.
 DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
 DR Activital; Cytokine; Glycoprotein; Hormone; Pregnancy; Signal.
 FT SIGNAL 1 23 By similarity.
 FT CHAIN 24 195 Interferon tau.
 FT DISULFID 24 122 By similarity.
 FT DISULFID 52 162 By similarity.
 FT CARBOHYD 101 101 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 195 AA; 22370 MW; 39599512F3C34208 CRC64;
 Query March 86.0%; Score 780; DB 1; Length 195;
 Best Local Similarity 87.2%; Pred. No. 2.1e-64;
 Matches 150; Conservative 6; Mismatches 16; Indels 0; Gaps 0;
 QY 1 CYLSRKLMPLDARENKLLDRMNRSLSPHSCQDRKDFGLPQEWVSGDQLQKDQAFVLYEM 60
 DB 24 CYLSRRRPTLDVRENLRLDRNRRLSPHSCQDRKDFGLPQEWVSGDQLQKDQALSVLYEM 83
 QY 61 LQGSFNLFTYHSAANDTTLLEQLCTGLQQLDHLDTCKGQVGEEDSELGMNDPIVTV 120
 DB 84 LQGFNFNFTYHSAANDTTLLEQLCTGLQQLDHLDTCKGQVGEEDSELGMNDPIVTV 143
 QY 121 KKTFFQGIYDYLQEKYSGSCAMEIYRVVMRRLATVSTTLQKRLTMGGDLNSP 172
 DB 144 KKTFFQGIYDYLQEKYSGSCAMEIYRVVMRRLATVSTTLQKRLTMGGDLNSP 195
 RESULT 19
 INTB SHEEP STANDARD; PRT; 195 AA.
 AC P28169;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interferon tau-11 precursor (IFN-tau11) (Trophoblast protein-1) (TP-1)
 DE (Trophoblastin) (Antilitheolysin) (Trophoblast antilitheolytic protein)
 DE (P4) (84).
 GN Name=IFNT11;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis
 OC NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92242937; PubMed=1374107;
 RA Leaman D.W., Roberts R.M.;
 RT Genes for the trophoblast interferons in sheep, goat, and musk ox and
 RT distribution of related genes among mammals.";
 RT J. Interferon Res. 12:1-11(1992).
 RL [2]
 RN FUNCTION.
 RX MEDLINE=6174804; PubMed=8603586; DOI=10.1210/en.137.3.1144;
 RA Spencer T.E., Bazer F.W.;
 RT Ovine interferon tau suppresses transcription of the estrogen
 RT receptor and oxytocin receptor genes in the ovine endometrium.";
 RL Endocrinology 137:1144-1147(1996).
 RN [3]
 RP CIRCULAR DIGROISM ANALYSIS, AND 3D-STRUCTURE MODELING.
 RX MEDLINE=95062134; PubMed=7971949;
 RA Jarpe M.A., Johnson H.M., Bazer F.W., Ott T.L., Curto E.V.,
 RA Krishna N.R., Pontzer C.H.;
 RT Predicted structural motif of IFN tau.";

RL Protein Eng. 7:863-867(1994).
 RN [4]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=96318252; PubMed=8746786;
 RA Senda T., Saiton S.-I., Mitsu Y., Li J., Roberts R.M.;
 RT "A three-dimensional model of interferon-tau.";
 RL J. Interferon Cytokine Res. 15:1053-1060(1995).
 RN [5]
 RP MUTAGENESIS.
 RX MEDLINE=95014251; PubMed=7929162;
 RA Li J., Roberts R.M.;
 RT "Structure-function relationships in the interferon-tau (IFN-tau).
 RT Changes in receptor binding and in antiviral and antiproliferative
 RT activities resulting from site-directed mutagenesis performed near the
 RT carboxyl terminus.";
 RL J. Biol. Chem. 269:24826-24833(1994).
 RN [6]
 RP MUTAGENESIS.
 RX MEDLINE=97156192; PubMed=9002652;
 RA Niswender K.D., Li J., Powell M.R., Loos K.R., Roberts R.M.,
 RA Kelsier D.H., Smith M.F.;
 RT "Effect of variants of interferon-tau with mutations near the carboxyl
 RT terminus on luteal life span in sheep.";
 RL Biol. Reprod. 56:214-220(1997).
 RN [7]
 RP REVIEW.
 RX MEDLINE=99081096; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
 RA Martal J.L., Chene N.M., Huynh L.P., L'Hartidon R.M., Renaud P.B.,
 RA Guillemot M.W., Charlier M.A., Charpigny S.Y.;
 RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-
 RT ubiquitous expression, structure-function relationships, a pregnancy
 RT hormonal embryonic signal and cross-species therapeutic
 RT potentialities.";
 RL Biochimie 80:755-777(1998).
 CC -1- FUNCTION: Paracrine hormone primarily responsible for maternal
 CC recognition of pregnancy. Interacts with endometrial receptors,
 CC probably type I interferon receptors, and blocks estrogen receptor
 CC expression, preventing the estrogen-induced increase in oxytocin
 CC receptor expression in the endometrium. This results in the
 CC suppression of the pulsatile endometrial release of the luteolytic
 CC hormone prostaglandin F2-alpha, hindering the regression of the
 CC corpus luteum (luteolysis) and therefore a return to ovarian
 CC cyclicity. This, and a possible direct effect of IFN-tau on
 CC prostaglandin synthesis, leads in turn to continued ovarian
 CC progesterone secretion, which stimulates the secretion by the
 CC endometrium of the nutrients required for the growth of the
 CC conceptus. In summary, displays particularly high antiviral and
 CC antiproliferative potency concurrently with particular weak
 CC cytotoxicity, high antilitheolytic activity and immunomodulatory
 CC properties. In contrast with other IFNs, IFN-tau is not virally
 CC inducible.
 CC -1- SUBCELLULAR LOCATION: Secreted into the uterine lumen.
 CC -1- TISSUE SPECIFICITY: Constitutively and exclusively expressed in
 CC the mononuclear cells of the extra-embryonic trophoctoderm.
 CC -1- DEVELOPMENTAL STAGE: Major secretory product synthesized by the
 CC sheep conceptus between days 13 and 21 of pregnancy.
 CC -1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from
 CC IFN-omega genes in the ruminantia suborder and have continued to
 CC duplicate independently in different lineages of the ruminantia.
 CC They encode for proteins very similar in sequence but with
 CC different biological potency and pattern of expression.
 CC -1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-
 CC alpha1 subfamily.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sb-sib.ch).
 CC -----
 DR EMBL; M73241; AAA31573.1; -.

DR PIR, I47097, I47097.
 DR HSBP, P01563, ZHIE.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR009471; Interferon_abd.
 DR Pfam; PF00143; Interferon; 1.
 DR PRINTS; PR00266; INTERFERONAB.
 DR ProDom; PD000550; Interferon_abd; 1.
 DR PROSITE; PS00252; INTERFERON_AB_D; 1.
 DR Anticviral; Cytokine; Glycoprotein; Hormone; Multigene family;
 KM Pregnancy; Signal.
 FT SIGNAL 1 23 By similarity.
 FT CHAIN 24 195 Interferon tau-11.
 FT DISULFID 24 122 By similarity.
 FT DISULFID 52 162 By similarity.
 FT CARBOHYD 101 101 N-linked (GlcNAc...) (potential).
 FT MUTAGEN 166 166 I->T: 20-fold reduction in receptor binding activity, greatly reduced antiviral and almost abolished antiproliferative activity.
 FT MUTAGEN 183 183 antiproliferative activity.
 FT MUTAGEN 183 183 Missing: Little effect on receptor binding activity but greatly reduced antiviral and almost abolished antiproliferative activity.
 FT MUTAGEN 185 195 Missing: Little effect on receptor binding activity but greatly reduced antiviral and almost abolished antiproliferative activity.
 FT SEQUENCE 195 AA; 22243 MW; DC6321E42BDF948A CRC64;
 SQ
 Query Match 85.8%; Score 778; DB 1; Length 195;
 Best Local Similarity 86.6%; Pred. No. 3.2e-64;
 Matches 149; Conservative 13; Mismatches 10; Indels 0; Gaps 0;
 QY 1 CYLSRKMLDARENLKLDKRNRLSPHSCLDRKDFGLPOEWEDEQLQKDAFPVLYEM 60
 Db 24 CYLSGRMLDARENLRLDRNRRLSPHSCLDRKDFGLPOEWEDEQLQKDAFPVLYEM 83
 QY 61 LQGSFNLFTYTHSSAAMDITLLEQLCTGLQOQLDHLDTGRCQVGEEDSEIGNDPIYTV 120
 Db 84 LQGSFNLFTYTHSSAAMDITLLEQLCTGLQOQLDHLDTGRCQVGEEDSEIGNDPIYTV 143
 QY 121 KKYFGCIYDLYOEKGYSCDCAWEIVVEMRALVTSTLOKRLTKVGGDLSNP 172
 Db 144 KKYFGCIYDLYOEKGYSCDCAWEIVVEMRALVTSTLOKRLTKVGGDLSNP 195
 RESULT 20
 INT1_BOVIN STANDARD; PRT; 195 AA.
 AC P15696; P15694; Q28126; Q28127; Q28128; Q28191; Q95NE2;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interferon tau-1 precursor (IFN-tau) (Trophoblast protein-1) (TP-1) (Trophoblastin) (Antiluteolysin) (Trophoblast antiluteolytic protein).
 GN Name=IFNT1;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovine; Bos
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A. (IFN-TAU1A AND IFN-TAU1D).
 RX MEDLINE=89127268; PubMed=2521687;
 RA Imkawa K., Hansen T.R., Malachy P.-V., Anthony R.V., Pollas H.G.,
 RA Marotz K.R., Roberts R.M.;
 RT "Molecular cloning and characterization of complementary
 RT deoxyribonucleic acids corresponding to bovine trophoblast protein-1:
 RT a comparison with ovine trophoblast protein-1 and bovine interferon-
 RT alpha II.";
 RL Mol. Endocrinol. 3:127-139(1989).
 RN [2]
 RP SEQUENCE FROM N.A. (IFN-TAU1C).

RC TISSUE=Trophoblast;
 RX MEDLINE=90334707; PubMed=2378676;
 RA Stewart H.J., McCan S.H., Flint A.P.F.;
 RT "Structure of an interferon-alpha 2 gene expressed in the bovine
 RT conceptus early in gestation.";
 RL J. Mol. Endocrinol. 4:275-282(1990).
 RN [3]
 RP SEQUENCE FROM N.A. (IFN-TAU1A; IFN-TAU1B AND IFN-TAU1D).
 RX MEDLINE=91131606; PubMed=1704373;
 RA Hansen T.R., Leaman D.W., Cross J.C., Mathialagan N., Bixby J.A.,
 RA Roberts R.M.;
 RT "The genes for the trophoblast interferons and the related interferon-
 RT alpha II possess distinct 5'-promoter and 3'-flanking sequences.";
 RL J. Biol. Chem. 266:3060-3067(1991).
 RN [4]
 RP SEQUENCE FROM N.A. (IFN-TAU1C).
 RC TISSUE=Trophoblast;
 RA Stewart H.J.;
 RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (INF-TAU1A).
 RA Roberts R.M.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (INF-TAU1C).
 RA Chung Y.G., Seidel G.E. Jr.;
 RT "Cloning bovine interferon-tau genes and characterizing their
 RT transcriptional expression during early pregnancy.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 24-195 FROM N.A. (IFN-TAU1C).
 RA Larson S.F., Liu L., Winkelman G.L., Kubisch H.M., Bixby J.A.,
 RA Roberts R.M., Ealy A.D.;
 RT "The expressed genes for bovine interferon-tau: identification and
 RT expression during conceptus development.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=96318252; PubMed=8746786;
 RA Senda T., Saitoh S.-I., Mitsui Y., Li J., Roberts R.M.;
 RT "A three-dimensional model of interferon-tau.";
 RL J. Interferon Cytokine Res. 15:1053-1060(1995).
 RN [9]
 RP REVIEW.
 RX MEDLINE=99081096; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
 RA Martal J.L., Chene N.M., Huynh L.P., L'Haxidon R.M., Reinaud P.B.,
 RA Guillomot M.W., Charlier M.A., Charpigny S.Y.;
 RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-
 RT ubiquitous expression, structure-function relationships, a pregnancy
 RT hormonal embryonic signal and cross-species therapeutic
 RT potentialities.";
 RL Biochimie 80:755-777(1998).
 CC -I- FUNCTION: Paracrine hormone primarily responsible for maternal
 CC recognition of pregnancy. Interacts with endometrial receptors,
 CC probably type I interferon receptors, and blocks estrogen receptor
 CC expression, preventing the estrogen-induced increase in oxytocin
 CC receptor expression in the endometrium. This results in the
 CC suppression of the pulsatile endometrial release of the luteolytic
 CC hormone prostaglandin F2-alpha, hindering the regression of the
 CC corpus luteum (luteolysis) and therefore a return to ovarian
 CC cyclicity. This, and a possible direct effect of IFN-tau on
 CC prostaglandin synthesis, leads in turn to continued ovarian
 CC progesterone secretion, which stimulates the secretion by the
 CC endometrium of the nutrients required for the growth of the
 CC conceptus. In summary, displays particularly high antiviral and
 CC antiproliferative potency concurrently with particular weak
 CC cytotoxicity, high antiluteolytic activity and immunomodulatory
 CC properties. In contrast with other IFNs, IFN-tau is not vitally
 CC inducible.
 CC -I- SUBCELLULAR LOCATION: Secreted into the uterine lumen.
 CC -I- TISSUE SPECIFICITY: Constitutively expressed in
 CC the mononuclear cells of the extra-embryonic trophoderm.
 CC -I- DEVELOPMENTAL STAGE: Major secretory product synthesized by the

```

CC bovine conceptus between days 15 and 25 of pregnancy.
CC -1- POLYMORPHISM: There seems to be four variants of IFN-tau 1: A, B
CC (shown here), C and D.
CC -1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from
CC IFN-omega genes in the ruminantia suborder and have continued to
CC duplicate independently in different lineages of the ruminantia.
CC They encode for proteins very similar in sequence but with
CC different biological potency and pattern of expression.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-
CC alpha11 subfamily.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements/
CC or send an email to license@ebi.ac.uk).
-----
DR EMBL; M31557; AAA50458.2; -
DR EMBL; M31556; AAA50457.1; -
DR EMBL; X65539; CAA46506.1; -
DR EMBL; M60903; AAB67325.1; -
DR EMBL; M60913; AAA62712.1; -
DR EMBL; M60908; AAA62711.1; -
DR EMBL; AF238612; AAG41469.1; -
DR EMBL; AF196320; AAF08671.2; -
DR PIR; A39505; A39505.
DR PIR; B39505; B39505.
DR PIR; S23751; S23751.
DR HSP; P56828; IBSL.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon_1.
DR PRINTS; PR00266; INTERFERONAB.
DR PROSITE; PS000550; Interferon_abd_1.
DR PROSITE; PS00252; INTERFERON_A_B_D_1.
KM Antiviral; Cytokine; Glycoprotein; Hormone; Multigene family;
KM Polymorphism; Pregnancy; Signal.
FT SIGNAL 1 23 Probable.
FT CHAIN 24 195 Interferon_tau-1.
FT DISULFID 24 122 By similarity.
FT FT 52 162 By similarity.
FT CARBOHYD 101 101 N-linked (GlcNAc...) (Potential).
FT VARIANT 29 29 D -> N (in IFN-tau1D).
FT VARIANT 88 88 F -> L (in IFN-tau1A).
FT VARIANT 169 169 V -> M (in IFN-tau1C and IFN-tau1D).
FT CONFLICT 18 18 P -> Q (in Ref. 1; AAA50458).
FT CONFLICT 20 20 R -> E (in Ref. 1; AAA50457).
SQ SEQUENCE 195 AA; 22134 MW; FP98CFAS4A86902 CRC64;
Query March 80.0%; Score 726; DB 1; Length 195;
Best Local Similarity 81.3%; Pred. No. 2.2e-59;
Matches 139; Conservative 13; Mismatches 19; Indels 0; Gaps 0;
QY 1 CYLSRKLMLDARENLKILDRNRLSPHSCLODRKDFGJPEWVGDLQKQAPVLYEM 60
DB 24 CYLSSEDMGAREVRLRLANRNRSHPICLODRKDFGLPEWVGNGDLQKQASVLYHEM 83
QY 61 LQGSFNLFTYEHSSAANDTLLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNDPIVTV 120
DB 84 LQGFNLFYTEHSSAANTTLLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNDPIVTV 143
QY 121 KKYFGQIVYDLOEGSYDCAWEIYRVEMRLVYTTLOKRLTGMGDLNS 171
DB 144 KKYFGQIVYDLOEGSYDCAWEIYRVEMRLVYTTLOKRLTGMGDLNS 194

```

```

DT 30-MAY-2000 (Rel. 39, last sequence update)
DE 05-JUL-2004 (Rel. 44, last annotation update)
DE Interferon_tau-2 (IFN-tau2) (trophoblast protein-1) (TP-1)
DE (trophoblastin) (Antitrolysin) (trophoblast antitrolytic protein).
GN Name=IFN2;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=91108971; Pubmed=11416010; DOI=10.1210/en.142.7.2906;
RA Ealy A.D., Larsen S.F., Liu L., Alexenko A.P., Winkelman G.L.,
RA Kudisch H.M., Bixby U.A., Roberts R.M.;
RT "Polymorphic forms of expressed bovine interferon-tau genes: relative
RT transcript abundance during early placental development, promoter
RT sequences of genes and biological activity of protein products.";
RL Endocrinology 142:2906-2915(2001).
RN [2]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=96318252; Pubmed=8746786;
RA Senda T., Saitoh S.-I., Mitsui Y., Li J., Roberts R.M.;
RT "A three-dimensional model of interferon-tau.";
RL J. Interferon Cytokine Res. 15:1053-1060(1995).
RN [3]
RP REVIEW.
RX MEDLINE=99081096; Pubmed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
RA Martal J.L., Chene N.M., Huynh L.P., L'Havard R.M., Reinard P.B.,
RA Guillouet M.W., Charlier M.A., Charliguy S.Y.;
RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-
RT ubiquitous expression, structure-function relationships, a pregnancy
RT hormonal embryonic signal and cross-species therapeutic
RT potentialities.";
RL Biochimie 80:755-777(1998).
CC -1- FUNCTION: Paracrine hormone primarily responsible for maternal
CC recognition of pregnancy. Interacts with endometrial receptors,
CC probably type I interferon receptors, and blocks estrogen receptor
CC expression, preventing the estrogen-induced increase in oxytocin
CC receptor expression in the endometrium. This results in the
CC suppression of the pulsatile endometrial release of the luteolytic
CC hormone prostaglandin F2-alpha, hindering the regression of the
CC corpus luteum (luteolysis) and therefore a return to ovarian
CC cyclicity. This, and a possible direct effect of IFN-tau on
CC prostaglandin synthesis, leads in turn to continued ovarian
CC progesterone secretion, which stimulates the secretion by the
CC endometrium of the nutrients required for the growth of the
CC conceptus. In summary, displays particularly high antiviral and
CC antiproliferative potency concurrently with particular weak
CC cytotoxicity, high antitrolytic activity and immunomodulatory
CC properties. In contrast with other IFNs, IFN-tau is not vitally
CC inducible.
CC -1- SUBCELLULAR LOCATION: Secreted into the uterine lumen.
CC -1- TISSUE SPECIFICITY: Constitutively and exclusively expressed in
CC the mononuclear cells of the extra-embryonic trophoderm.
CC -1- DEVELOPMENTAL STAGE: Major secretory product synthesized by the
CC bovine conceptus between days 15 and 25 of pregnancy.
CC -1- POLYMORPHISM: There seems to be three variants of IFN-tau 2: A
CC (shown here), B and C.
CC -1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from
CC IFN-omega genes in the ruminantia suborder and have continued to
CC duplicate independently in different lineages of the ruminantia.
CC They encode for proteins very similar in sequence but with
CC different biological potency and pattern of expression.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-
CC alpha11 subfamily.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial

```


RESULT 24
INT3 BOVIN
ID INT3 BOVIN STANDARD: PRT; 172 AA.
AC P56831; Q9M209;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interferon tau-3 (IFN-tau3) (Trophoblast protein-1) (TP-1)
DE (Trophoblastin) (Antitrobleysin) (Trophoblast antileukolytic protein).
GN Name=IFN3;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A. (IFN-TAU3A; IFN-TAU3B; IFN-TAU3C AND IFN-TAU3D).
RC TISSUE=Blasocyt; and Embryo;
RA Larson S.F., Liu L., Winkelman G.L., Kubisch H.M., Bixby J.A.,
RA Roberts R.M., Baly A.D.;
RT "The expressed genes for bovine interferon-tau: identification and
RT expression during conceptus development.";
RT Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (IFN-TAU3E).
RC TISSUE=Blasocyt;
RA Larson S.F., Liu L., Winkelman G.L., Kubisch H.M., Alexenko A.P.,
RA Bixby J.A., Roberts R.M., Baly A.D.;
RT "Polymorphisms among the expressed genes for bovine interferon-tau:
RT identification and expression during early placental development.";
RT Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
RN [3]
RP 3D-STRUCTURE MODELING.
RA MEDLINE=96318252; PubMed=8746786;
RA Senda T., Saitoh S.-I., Mitsui Y., Li J., Roberts R.M.;
RT "A three-dimensional model of interferon-tau";
RT J. Interferon Cytokine Res. 15:1053-1060(1995).
RN [4]
RP REVIEW.
RA MEDLINE=99081096; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
RA Maccall J.L., Chene N.M., Huynh L.P., L'Hardon R.M., Renaud P.B.,
RA Guillouet M.W., Charlier M.A., Chapigny S.Y.;
RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-
RT ubiquitous expression, structure-function relationships, a pregnancy
RT potentialities";
RT Biochimie 80:755-777(1998).
RL
CC -1- FUNCTION: Paracrine hormone primarily responsible for maternal
CC recognition of pregnancy. Interacts with endometrial receptors,
CC probably type I interferon receptors, and blocks estrogen receptor
CC expression, preventing the estrogen-induced increase in oxytocin
CC receptor expression in the endometrium. This results in the
CC suppression of the pulsatile endometrial release of the leukolytic
CC hormone prostaglandin F2-alpha, hindering the regression of the
CC corpus luteum (luteolysis) and therefore a return to ovarian
CC cyclicity. This, and a possible direct effect of IFN-tau on
CC prostaglandin synthesis, leads in turn to continued ovarian
CC progesterone secretion, which stimulates the secretion by the
CC endometrium of the nutrients required for the growth of the
CC conceptus. In summary, displays particularly high antiviral and
CC antiproliferative potency concurrently with particular weak
CC cytotoxicity, high antileukolytic activity and immunomodulatory
CC properties. In contrast with other IFNs, IFN-tau is not vitally
CC inducible.
CC -1- SUBCELLULAR LOCATION: Secreted into the uterine lumen.
CC -1- TISSUE SPECIFICITY: Constitutively and exclusively expressed in
CC the mononuclear cells of the extra-embryonic trophoctoderm.
CC -1- DEVELOPMENTAL STAGE: Major secretory product synthesized by the
CC bovine conceptus between days 15 and 25 of pregnancy.
CC -1- POLYMORPHISM: There seems to be five variants of IFN-tau 3: A
CC (shown here), B, C, D and E.

CC -1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from
CC IFN-omega genes in the ruminantia suborder and have continued to
CC duplicate independently in different lineages of the ruminantia.
CC They encode for proteins very similar in sequence but with
CC different biological potency and pattern of expression.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-
CC alpha1 subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; AF196324; AAF08675.1; -;
CC DR EMBL; AF196325; AAF08676.1; -;
CC DR EMBL; AF196326; AAF08677.1; -;
CC DR EMBL; AF196327; AAF08678.1; -;
CC DR EMBL; AF270471; AAF74783.1; -;
CC DR HSSP; P56828; 1BSL.
CC DR InterPro; IPR009079; 4_helix_cytokine.
CC DR InterPro; IPR000471; Interferon_abd.
CC DR Pfam; PF00143; Interferon_1.
CC DR PRINTS; PR000550; INTERFERONAB.
CC DR PRODOM; PD000550; Interferon_abd.1.
CC DR PROSITE; PS00252; INTERFERON_A_B_D; FALSE_NEG.
CC KW Antiviral; Cytokine; Glycoprotein; Hormone; Multigene family;
CC KM Polymorphism; Pregnancy.
CC FT DISULFID 1 99 By similarity.
FT DISULFID 29 139 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 78 78
FT VARIANT 25 25 A -> P (in IFN-tau3D).
FT VARIANT 76 76 A -> S (in IFN-tau3B).
FT VARIANT 126 126 D -> G (in IFN-tau3E).
FT VARIANT 129 129 V -> A (in IFN-tau3C).
FT VARIANT 146 146 V -> M (in IFN-tau3E).
SQ SEQUENCE 172 AA; 19774 MW; B02F38A09C388653 CRC64;

Query Match 77.9%; Score 707; DB 1; Length 172;
Best Local Similarity 79.5%; Pred. No. 1,le-57;
Matches 136; Conservative 13; Mismatches 22; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARPKILDMNRLSPHSCLQDRKDFGLPEWVGDLQKQAPVLYEM 60
Db 1 CYLSEDMGLARENLRLLARKNRLSPHPCLDKRDFFLPQEWVGSQLQKQDAISVLHEM 60
QY 61 LQCSFNLFTYEHSSAAMDITLLLEQLCTGLQOQDLHDLPTCRGOVWGEEDSELGNMPTVTV 120
Db 61 LQCCFNFLFHLBSSAAMNTLLLEQLCTGLQOQDLHDLPTCRGOVWGEEDSELGNMPTVTV 120
QY 121 KKYFQGIYDYLQEKYSGDCAMEIVRWVMPALVSTTLQKRLTVMGDLNS 171
Db 121 KKYFQDIHYVLKEKREYSDCAMEIIRVEMRALSSTTLQKRLRMGDLNS 171

RESULT 25
Q9GLI6
ID Q9GLI6 PRELIMINARY; PRT; 195 AA.
AC Q9GLI6;
DT 01-MAR-2001 (TREMUREl. 16, Created)
DT 01-MAR-2001 (TREMUREl. 16, Last sequence update)
DT 01-MAR-2004 (TREMUREl. 26, Last annotation update)
DE Interferon tau.
GN Name=IFN-tau-c3;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.

RA Chung Y.G., Seidel G.E. Jr.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
 DR EMBL: AF238611; GenBank: AF238611; RefSeq: AF238611.1;
 DR PIR: A40068; A40068.
 DR HSRP: P56828; IBSL.
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0005126; F:hematopoietin/interferon-c-class (D200-domain. . .); IEA.
 DR GO: GO:0006952; P:defense response; IEA.
 DR InterPro: IPR009079; 4_helix_cytokine.
 DR InterPro: IPR00471; Interferon_abd.
 DR Pfam: PF00143; Interferon_1.
 DR PRINTS: PR00266; INTERFERONAB.
 DR ProDom: PD000550; Interferon_abd; 1.
 DR SMART: SM00076; IFabd; 1.
 DR Antiviral: Cytokine.
 KM Antiviral: Cytokine.
 SQ SEQUENCE 195 AA; 22160 MW; 6DB1FAE39BF033FA CRC64;

Query Match 77.4%; Score 702; DB 2; Length 195;
 Best Local Similarity 78.9%; Pred. No. 3.7e-57;
 Matches 135; Conservative 13; Mismatches 23; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENKLLDRNRRLSPHSCLODRKDFGLPQEMVEGDQLQKQDAFPVLYEM 60
 |||||
 DB 24 CYLSEDMHLAGRENRLRLAQRNRLSPHSCLODRKDFGLPQEMVEGDQLQKQDAISVLHEM 83
 |||||

QY 61 LQGFNLFYTHSSAANDTLLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNDDPIVTV 120
 |||||
 DB 84 LQGFNLFYTHSSAANDTLLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNDDPIVTV 143
 |||||

QY 121 KKYFGIYDIYLOEKGYSDCAWEIVRVMRALTSTLQKRLTKMGGLNS 171
 |||||
 DB 144 KKYFQIHVILYKKEYSDCAMEIIRVEMRLSSSTLQKRLTKMGGLNS 194
 |||||

RESULT 26
 Q6DUN3 PRELIMINARY; PRT; 172 AA.
 ID Q6DUN3
 AC Q6DUN3;
 DT 25-OCT-2004 (TREMblrel. 28; Created)
 DT 25-OCT-2004 (TREMblrel. 28; Last sequence update)
 DT 25-OCT-2004 (TREMblrel. 28; Last annotation update)
 DE Interferon tau2 (Fragment).
 OS Bison bison (American bison).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bison.
 OX NCBI_TaxID=9901;
 RN [1]
 RM SEQUENCE FROM N.A.
 RA Raemussen T.A., Ealy A.D., Kubisch H.M.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
 DR EMBL: AY63747; AAT67216.1; -
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0005126; F:hematopoietin/interferon-c-class (D200-domain. . .); IEA.
 DR GO: GO:0006952; P:defense response; IEA.
 DR InterPro: IPR009079; 4_helix_cytokine.
 DR InterPro: IPR00471; Interferon_abd.
 DR Pfam: PF00143; Interferon_1.
 DR PRINTS: PR00266; INTERFERONAB.
 DR ProDom: PD000550; Interferon_abd; 1.
 DR SMART: SM00076; IFabd; 1.
 DR Antiviral: Cytokine.
 FT NON_TER 1
 FT NON_TER 172
 SQ SEQUENCE 172 AA; 19764 MW; 7E41012B093889E1 CRC64;

Query Match 76.7%; Score 696; DB 2; Length 172;
 Best Local Similarity 78.4%; Pred. No. 1.1e-56;
 Matches 134; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENKLLDRNRRLSPHSCLODRKDFGLPQEMVEGDQLQKQDAFPVLYEM 60
 |||||
 DB 24 CYLSEDMHLAGRENRLRLAQRNRLSPHSCLODRKDFGLPQEMVEGDQLQKQDAISVLHEM 83
 |||||

QY 61 LQGFNLFYTHSSAANDTLLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNDDPIVTV 120
 |||||
 DB 84 LQGFNLFYTHSSAANDTLLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNDDPIVTV 143
 |||||

QY 121 KKYFGIYDIYLOEKGYSDCAWEIVRVMRALTSTLQKRLTKMGGLNS 171
 |||||
 DB 144 KKYFQIHVILYKKEYSDCAMEIIRVEMRLSSSTLQKRLTKMGGLNS 194
 |||||

DB 1 CYLSEDMHLAGRENRLRLAQRNRLSPHSCLODRKDFGLPQEMVEGDQLQKQDAISVLHEM 60
 |||||
 QY 61 LQGFNLFYTHSSAANDTLLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNDDPIVTV 120
 |||||
 DB 61 LQGFNLFYTHSSAANDTLLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNDDPIVTV 120
 |||||

QY 121 KKYFGIYDIYLOEKGYSDCAWEIVRVMRALTSTLQKRLTKMGGLNS 171
 |||||
 DB 121 KKYFQIHVILYKKEYSDCAMEIIRVEMRLSSSTLQKRLTKMGGLNS 171
 |||||

RESULT 27
 Q9GLLS PRELIMINARY; PRT; 195 AA.
 ID Q9GLLS
 AC Q9GLLS;
 DT 01-MAR-2001 (TREMblrel. 16; Created)
 DT 01-MAR-2001 (TREMblrel. 16; Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 26; Last annotation update)
 DE Interferon tau.
 OS Bos taurus (Bovine).
 OS Name=IFN-tau-cl;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RM SEQUENCE FROM N.A.
 RA Chung Y.G., Seidel G.E. Jr.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
 DR EMBL: AF238613; AAG14170.1; -
 DR HSRP: P56828; IBSL.
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0005126; F:hematopoietin/interferon-c-class (D200-domain. . .); IEA.
 DR GO: GO:0006952; P:defense response; IEA.
 DR InterPro: IPR009079; 4_helix_cytokine.
 DR InterPro: IPR00471; Interferon_abd.
 DR Pfam: PF00143; Interferon_1.
 DR PRINTS: PR00266; INTERFERONAB.
 DR ProDom: PD000550; Interferon_abd; 1.
 DR SMART: SM00076; IFabd; 1.
 DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
 KM Antiviral: Cytokine.
 SQ SEQUENCE 195 AA; 22139 MW; 689C2443B203E50A CRC64;

Query Match 76.4%; Score 693; DB 2; Length 195;
 Best Local Similarity 78.4%; Pred. No. 2.5e-56;
 Matches 134; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENKLLDRNRRLSPHSCLODRKDFGLPQEMVEGDQLQKQDAFPVLYEM 60
 |||||
 DB 24 CYLSEDMHLAGRENRLRLAQRNRLSPHSCLODRKDFGLPQEMVEGDQLQKQDAISVLHEM 83
 |||||

QY 61 LQGFNLFYTHSSAANDTLLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNDDPIVTV 120
 |||||
 DB 84 LQGFNLFYTHSSAANDTLLLEQLCTGLQOQLDHLDTCRGQVNGEEDSELGNDDPIVTV 143
 |||||

QY 121 KKYFGIYDIYLOEKGYSDCAWEIVRVMRALTSTLQKRLTKMGGLNS 171
 |||||
 DB 144 KKYFQIHVILYKKEYSDCAMEIIRVEMRLSSSTLQKRLTKMGGLNS 194
 |||||

RESULT 28
 INT GIRCA STANDARD; PRT; 195 AA.
 ID INT GIRCA
 AC Q95187;
 DT 30-MAY-2000 (Rel. 39; Created)
 DT 30-MAY-2000 (Rel. 39; Last sequence update)
 DT 05-JUN-2004 (Rel. 44; Last annotation update)
 DE Interferon tau precursor (IFN-tau) (Trophoblast protein-1) (TP-1)
 DE (Trophoblastin) (Antiluteolysin) (Trophoblast antiluteolytic protein).
 GN Name=IFNT;

OS Giraffe camelopardalis (Giraffe).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Giraffidae;
 CC Giraffe.
 CC NCBI_TaxID=9894;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97093009; PubMed=8938571;
 RA Liu L., Leaman D.W., Roberts R.M.;
 RT "The interferon-tau genes of the giraffe, a nonbovid species."
 RL Interferon Cytokine Res. 15:943-951(1996).
 CC -1- FUNCTION: Paracrine hormone primarily responsible for maternal
 CC recognition of pregnancy. Interacts with endometrial receptors,
 CC probably type I interferon receptors, and blocks estrogen receptor
 CC expression, preventing the estrogen-induced increase in oxytocin
 CC receptor expression in the endometrium. This results in the
 CC suppression of the pulsatile endometrial release of the luteolytic
 CC hormone prostaglandin F2-alpha, hindering the regression of the
 CC corpus luteum (luteolysis) and therefore a return to ovarian
 CC cyclicity. This, and a possible direct effect of IFN-tau on
 CC prostaglandin synthesis, leads in turn to continued ovarian
 CC progesterone secretion, which stimulates the secretion by the
 CC endometrium of the nutrients required for the growth of the
 CC conceptus. In summary, displays particularly high antiviral and
 CC antiproliferative potency concurrently with particularly weak
 CC cytotoxicity, high antiluteolytic activity and immunomodulatory
 CC properties. In contrast with other IFNs, IFN-tau is not virally
 CC inducible (by similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted into the uterine lumen.
 CC -1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-
 CC alpha1 subfamily.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U55050; AAA99814.1; -.
 DR HSSP; P56828; 185L.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR000471; Interferon_abd.
 DR Pfam; PF00143; Interferon; 1.
 DR PRINTS; PR00266; INTERFERONAB.
 DR PRODOM; PD000550; Interferon_abd; 1.
 DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
 KW Antiviral; Cytokine; Hormone; Pregnancy; Signal.
 FT SIGNAL 1 23 By similarity.
 FT CHAIN 24 195 Interferon tau.
 FT DISULFID 52 162 By similarity.
 FT DISULFID 87 109 Potential.
 SO SEQUENCE 195 AA; 22046 MW; 5073f22bfb45d8a CRC64;
 Query Match 74.9%; Score 679; DB 1; Length 195;
 Best Local Similarity 75.6%; Pred. No. 5e-55;
 Matches 130; Conservative 18; Mismatches 24; Indels 0; Gaps 0;

INT CEREL
 ID INT CEREL STANDARD; PRT; 195 AA.
 AC 046633;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interferon tau precursor (IFN-tau) (Trophoblast protein-1) (TP-1)
 GN (Trophoblastin) (Antiluteolytic) (Trophoblast antiluteolytic protein).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
 CC Cervinae; Cervus.
 CC NCBI_TaxID=9860;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99273269; PubMed=10341723;
 RA Demmers K.J., Kaluz S., Deakin D.W., Jabbour H.N., Flint A.P.F.;
 RT "Production of interferon by the conceptus in red deer Cervus
 RT elaphus."
 RL J. Reprod. Fertl. 115:59-65(1999).
 RN [2]
 RP REVIEW.
 RX MEDLINE=99081036; PubMed=9865498; DOI=10.1016/S0300-9084(99)80029-7;
 RA Martal J.L., Chene N.M., Huynh L.P., L'Hardion R.M., Reinaud P.B.,
 RA Guillomot M.W., Charlier M.A., Charpigny S.Y.;
 RT "IFN-tau: a novel subtype I IFN. Structural characteristics, non-
 RT ubiquitous expression, structure-function relationships, a pregnancy
 RT hormonal embryonic signal and cross-species therapeutic
 RT potentialities."
 RL Biochimie 80:755-777(1998).
 CC -1- FUNCTION: Paracrine hormone primarily responsible for maternal
 CC recognition of pregnancy. Interacts with endometrial receptors,
 CC probably type I interferon receptors, and blocks estrogen receptor
 CC expression, preventing the estrogen-induced increase in oxytocin
 CC receptor expression in the endometrium. This results in the
 CC suppression of the pulsatile endometrial release of the luteolytic
 CC hormone prostaglandin F2-alpha, hindering the regression of the
 CC corpus luteum (luteolysis) and therefore a return to ovarian
 CC cyclicity. This, and a possible direct effect of IFN-tau on
 CC prostaglandin synthesis, leads in turn to continued ovarian
 CC progesterone secretion, which stimulates the secretion by the
 CC endometrium of the nutrients required for the growth of the
 CC conceptus. In summary, displays particularly high antiviral and
 CC antiproliferative potency concurrently with particularly weak
 CC cytotoxicity, high antiluteolytic activity and immunomodulatory
 CC properties. In contrast with other IFNs, IFN-tau is not virally
 CC inducible.
 CC -1- SUBCELLULAR LOCATION: Secreted into the uterine lumen.
 CC -1- TISSUE SPECIFICITY: Constitutively and exclusively expressed in
 CC the mononuclear cells of the extra-embryonic trophoderm.
 CC -1- DEVELOPMENTAL STAGE: Major secretory product synthesized by the
 CC conceptus during a very short period in early pregnancy.
 CC -1- MISCELLANEOUS: IFN-tau genes are intronless. They evolved from
 CC IFN-omega genes in the ruminantia suborder and have continued to
 CC duplicate independently in different lineages of the ruminantia.
 CC They encode for proteins very similar in sequence but with
 CC different biological potency and pattern of expression.
 CC -1- SIMILARITY: Belongs to the alpha/beta interferon family. IFN-
 CC alpha1 subfamily.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; A000638; CA04193.1; -.
 DR HSSP; P56828; 185L.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR000471; Interferon_abd.

```

DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR PRODOM; PD000550; Interferon abd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine; Hormone; Pregnancy; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 195 Interferon tau.
FT DISULFID 24 122 By similarity.
FT DISULFID 52 162 By similarity.
SQ SEQUENCE 195 AA; 22075 MW; F5304ACB1ACFOCC7 CRC64;

Query Match 72.0%; Score 653; DB 1; Length 195;
Best Local Similarity 75.6%; Pred. No. 1.3e-52;
Matches 130; Conservative 13; Mismatches 29; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENILKLDNRNRLSPHSCLDRKDFGLPQEMVEGDLQKQAFPVLYEM 60
DB 24 CDLSQNHVLFGRKRLILGQWTRLSPRFCLODRKDFGLPQEMVEGDLQKQAFVLYHEM 83
QY 61 LQGSFNLFTYTHSSAANDTTLLBQLCTGLQOQLDHLDTCRGQWGEEDSEIGNDPITYV 120
DB 84 LQGSFNLFTYTHSSAANDTTLLBQLCTGLQOQLDHLDTCRGQWGEEDSEIGNDPITYV 143
QY 121 KKYFGIYDYLQEGYSDCAWEIVRVMRALTVSTTLQKRLTKMGDGLNSP 172
DB 144 KKYFGIHYVLYQEKGYSDCAWEIVRVMRALTVSTTLQKRLTKMGDGLNSP 195

RESULT 30
INDL HUMAN STANDARD; PRT; 195 AA.
ID _INDL_HUMAN
AC P37290;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE Interferon delta-1 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94193794; Pubmed=751610;
RA Whaley A.E., Meka C.S.R., Reddy C.S., Harbison L.A., Hunt J.S.,
RA Imakawa K.;
RT "Identification and cellular localization of unique interferon mRNA
RT from human placenta."
RL J. Biol. Chem. 269:10864-10868(1994).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L25664; AAA36123.1; -.
DR PIR; A53746; A53746.
DR HSSP; P56828; 1BSL.
DR GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .); NAS.
DR GO; GO:0009615; P:response to virus; NAS.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR PRODOM; PD000550; Interferon abd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine; Glycoprotein; Multigene family; Signal.
FT SIGNAL 1 23 Potential.

```

```

FT CHAIN 24 195 Interferon delta-1.
FT DISULFID 24 122 By similarity.
FT DISULFID 52 162 By similarity.
SQ SEQUENCE 195 AA; 21698 MW; BE1CFEE2E2E29165 CRC64;

Query Match 67.1%; Score 609; DB 1; Length 195;
Best Local Similarity 68.6%; Pred. No. 1.6e-48;
Matches 118; Conservative 20; Mismatches 34; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENILKLDNRNRLSPHSCLDRKDFGLPQEMVEGDLQKQAFPVLYEM 60
DB 24 CDLSQNHVLFGRKRLILGQWTRLSPRFCLODRKDFGLPQEMVEGDLQKQAFVLYHEM 83
QY 61 LQGSFNLFTYTHSSAANDTTLLBQLCTGLQOQLDHLDTCRGQWGEEDSEIGNDPITYV 120
DB 84 LQGSFNLFTYTHSSAANDTTLLBQLCTGLQOQLDHLDTCRGQWGEEDSEIGNDPITYV 143
QY 121 KKYFGIYDYLQEGYSDCAWEIVRVMRALTVSTTLQKRLTKMGDGLNSP 172
DB 144 KKYFGIHYVLYQEKGYSDCAWEIVRVMRALTVSTTLQKRLTKMGDGLNSP 195

RESULT 31
Q7M2Y7 PRELIMINARY; PRT; 195 AA.
ID Q7M2Y7
AC Q7M2Y7;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Interferon alpha-II-10 precursor.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92324492; Pubmed=1820971; DOI=10.1016/0303-7207(91)90270-3;
RA Charlier M., Hue D., Boissard M., Martal J., Gaye P.;
RT "Cloning and structural analysis of two distinct families of ovine
RT interferon-alpha genes encoding functional class II and trophoblast
RT (crt) alpha-interferons."
RL Mol. Cell. Endocrinol. 76:161-171(1991).
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
CC -----
DR PIR; A61403; A61403.
DR HSSP; P56828; 1BSL.
DR GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .); IEA.
DR GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .); IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR PRODOM; PD000550; Interferon abd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine.
SQ SEQUENCE 195 AA; 21642 MW; FFC53626BF5042B CRC64;

Query Match 67.0%; Score 608; DB 2; Length 195;
Best Local Similarity 69.2%; Pred. No. 2e-48;
Matches 119; Conservative 20; Mismatches 33; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENILKLDNRNRLSPHSCLDRKDFGLPQEMVEGDLQKQAFPVLYEM 60
DB 24 CDLSQNHVLFGRKRLILGQWTRLSPRFCLODRKDFGLPQEMVEGDLQKQAFVLYHEM 83
QY 61 LQGSFNLFTYTHSSAANDTTLLBQLCTGLQOQLDHLDTCRGQWGEEDSEIGNDPITYV 120
DB 84 LQGSFNLFTYTHSSAANDTTLLBQLCTGLQOQLDHLDTCRGQWGEEDSEIGNDPITYV 143
QY 121 KKYFGIYDYLQEGYSDCAWEIVRVMRALTVSTTLQKRLTKMGDGLNSP 172
DB 144 KKYFGIHYVLYQEKGYSDCAWEIVRVMRALTVSTTLQKRLTKMGDGLNSP 195

```

```

RESULT 32
P28170 PRELIMINARY; PRT; 195 AA.
ID P28170;
AC P28170;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Interferon omega.
GN Name=IFN-omega.
OS Ovis aries (sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92242937; PubMed=1374107;
RA Leaman D.W., Roberts R.M.;
RT "Genes for the trophoblast interferons in sheep, goat, and musk ox and
RT distribution of related genes among mammals.";
RL J. Interferon Res. 12:1-11(1992).
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
DR EMBL; M73245; AAA31507.1; -.
DR PIR; I47070; I47070.
DR HSSP; P56828; 1B5L.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR PRODOM; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
DR Antiviral; Cytokine.
SQ SEQUENCE 195 AA; 21732 MW; 42EF83B80EE26496 CRC64;

Query Match 64.7%; Score 587; DB 2; Length 195;
Best Local Similarity 67.4%; Pred. No. 1.8e-46;
Matches 116; Conservative 20; Mismatches 36; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENKILDRMRLSPHSCLQDRKDFGLPEBMVEGDLQKQAFPLYEM 60
AC P07352;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interferon omega-1 precursor (Interferon alpha-II-1) (IFN-omega-c1).
GN Name=IFN1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=65187974; PubMed=2985969;
RA Capon D.J., Shepard H.W., Goeddel D.V.;
RT "Two distinct families of human and bovine interferon-alpha genes are
RT coordinately expressed and encode functional polypeptides.";
RL Mol. Cell. Biol. 5:768-779(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX Chung Y.G., Seidel G.E. Jr.;
RT "Cloning bovine interferon-tau genes and characterizing their
RT transcriptional expression during early pregnancy.";
RL Submitted (FE8-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.

```

```

RC TISSUE=Embryo;
RX MEDLINE=93250155; PubMed=8485241;
RA Nephew K.P., Whaley A.E., Christenson R.K., Imakawa K.;
RT "Differential expression of distinct mRNAs for ovine trophoblast
RT protein-1 and related sheep type I interferons.";
RL Biol. Reprod. 48:768-778(1993).
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
DR EMBL; X59067; CAA41790.1; -.
DR PIR; I46397; I46397.
DR HSSP; P56828; 1B5L.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR PRODOM; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
DR Antiviral; Cytokine; Signal.
FT SIGNAL 1
FT CHAIN 24
FT SEQUENCE 195 AA; 21758 MW; 58335195CB7E1448 CRC64;

Query Match 64.5%; Score 585; DB 2; Length 195;
Best Local Similarity 66.9%; Pred. No. 2.7e-46;
Matches 115; Conservative 20; Mismatches 37; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENKILDRMRLSPHSCLQDRKDFGLPEBMVEGDLQKQAFPLYEM 60
AC P07352;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interferon omega-1 precursor (Interferon alpha-II-1) (IFN-omega-c1).
GN Name=IFN1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=65187974; PubMed=2985969;
RA Capon D.J., Shepard H.W., Goeddel D.V.;
RT "Two distinct families of human and bovine interferon-alpha genes are
RT coordinately expressed and encode functional polypeptides.";
RL Mol. Cell. Biol. 5:768-779(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX Chung Y.G., Seidel G.E. Jr.;
RT "Cloning bovine interferon-tau genes and characterizing their
RT transcriptional expression during early pregnancy.";
RL Submitted (FE8-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.

```

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/>
 CC or send an email to license@ebi.ac.uk).

CC -----

DR EMBL; M1002; AAA30578.1; -.
 DR EMBL; AF238610; AAG14167.1; -.
 DR PIR; B23285; IVE011.
 DR HSSP; P56828; IBSL.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR000471; Interferon_abd.
 DR Pfam; PF00143; Interferon_1.
 DR PRINTS; PR00266; INTERFERONAB.
 DR ProDom; PD000550; Interferon_abd; 1.
 DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
 DR Antiviral; Cytokine; Multigene family; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 195 Interferon omega-1.
 FT DISULFID 24 122 By similarity.
 FT DISULFID 52 162 By similarity.
 SQ SEQUENCE 195 AA; 21980 MM; 1865FD4BCAB2A15 CRC64;

Query Match 64.2%; Score 582; DB 1; Length 195;
 Best Local Similarity 66.9%; Pred. No. 5.2e-46;
 Matches 115; Conservative 18; Mismatches 39; Indels 0; Gaps 0;

Qy 1 CYLSRKMLDAREVLTLLDRNRRLSPHSCLODRKDFGLPQEMVGGDLOKQAPVLYEM 60
 Db CDSLNHVLGRQRLRLGQRRSPRCLODRKDFAPQEMVVSQFQKQALSVLHEM 83

Qy 61 LQGSFNLFTYEHSSAANDTTLLEQLCTGLQOQLDHLDTCRQVWGEEDSELGNNDPIVTV 120
 Db LQGSFNLFTYEHSSAANDTTLLEQLCTGLQOQLDHLDTCRQVWGEEDSELGNNDPIVTV 143

Qy 84 LQGSFNLFTYEHSSAANDTTLLEQLCTGLQOQLDHLDTCRQVWGEEDSELGNNDPIVTV 120
 Db LQGSFNLFTYEHSSAANDTTLLEQLCTGLQOQLDHLDTCRQVWGEEDSELGNNDPIVTV 143

Qy 121 KKYFQGIYDVLQEGYSDCAMEIVRVMRALVTSTLQKRLTMGGLNSP 172
 Db 144 KRYFQGIYDVLQEGYSDCAMEIVRVMRALVTSTLQKRLTMGGLNSP 195

RESULT 35
 Q6SMO8 PRELIMINARY; PRT; 129 AA.
 ID Q6SMO8
 AC Q6SMO8
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Interferon-cauza (Fragment).
 OS Bos mutus grunniens (Yak).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovine; Bos.
 CC NCBI_Taxid=30521;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA L1 Y., L1 N., L1 S.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
 DR EMBL; AY455289; AAR19064.1; -.
 DR HSSP; P56828; IBSL.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR000471; Interferon_abd.
 DR Pfam; PF00143; Interferon_1.
 DR PRINTS; PR00266; INTERFERONAB.
 DR ProDom; PD000550; Interferon_abd; 1.
 DR SMART; SM00076; Ipadb; 1.
 DR Antiviral; Cytokine. 1
 FT CHAIN 1 1
 NON_TER 1

FT NON TER 129 129
 SQ SEQUENCE 129 AA; 14764 MM; DA6E297C8CB0AB89 CRC64;

Query Match 58.5%; Score 531; DB 2; Length 129;
 Best Local Similarity 80.2%; Pred. No. 1.7e-41;
 Matches 101; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Qy 8 MLDAREVLTLLDRNRRLSPHSCLODRKDFGLPQEMVGGDLOKQAPVLYEM 67
 Db MLDAREVLTLLDRNRRLSPHSCLODRKDFGLPQEMVGGDLOKQAPVLYEM 63

Qy 68 FYTEHSSAANDTTLLEQLCTGLQOQLDHLDTCRQVWGEEDSELGNNDPIVTVKKYRQGI 127
 Db FYTEHSSAANDTTLLEQLCTGLQOQLDHLDTCRQVWGEEDSELGNNDPIVTVKKYRQGI 123

Qy 128 YDYLQE 133
 Db 124 HVTLYKE 129

RESULT 36
 Q29085 PRELIMINARY; PRT; 190 AA.
 ID Q29085
 AC Q29085
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE PolFN-alpha II-5 protein precursor.
 GN Name=PolFN-alpha II-5;
 OS Sus scrofa (Pig).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 CC NCBI_Taxid=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=domestica; Tissue=liver;
 RC MEDLINE=92193688; PubMed=1800582;
 RA Lettve F., La Bonnardiere C., Mege D.;
 RT "The porcine family of interferon-omega: cloning, structural analysis
 RT and functional studies of five related genes."
 RL J. Interferon Res. 11:341-350(1991).
 CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
 DR EMBL; X57196; CAA40482.1; -.
 DR PIR; S23711; S23711.
 DR HSSP; P56828; IBSL.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR000471; Interferon_abd.
 DR Pfam; PF00143; Interferon_1.
 DR PRINTS; PR00266; INTERFERONAB.
 DR ProDom; PD000550; Interferon_abd; 1.
 DR SMART; SM00076; Ipadb; 1.
 DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
 DR Antiviral; Cytokine; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 190 Interferon-alpha II-5.
 SQ SEQUENCE 190 AA; 21667 MM; D4BAC635AB3E207A CRC64;

Query Match 56.6%; Score 513.5; DB 2; Length 190;
 Best Local Similarity 62.0%; Pred. No. 1.2e-39;
 Matches 106; Conservative 24; Mismatches 36; Indels 5; Gaps 1;

Qy 1 CYLSRKMLDAREVLTLLDRNRRLSPHSCLODRKDFGLPQEMVGGDLOKQAPVLYEM 60
 Db CDSLNHVLGRQRLRLGQRRSPRCLODRKDFAPQEMVVSQFQKQALSVLHEM 83

Qy 61 LQGSFNLFTYEHSSAANDTTLLEQLCTGLQOQLDHLDTCRQVWGEEDSELGNNDPIVTV 120
 Db LQGSFNLFTYEHSSAANDTTLLEQLCTGLQOQLDHLDTCRQVWGEEDSELGNNDPIVTV 143

Qy 84 LQGSFNLFTYEHSSAANDTTLLEQLCTGLQOQLDHLDTCRQVWGEEDSELGNNDPIVTV 120
 Db LQGSFNLFTYEHSSAANDTTLLEQLCTGLQOQLDHLDTCRQVWGEEDSELGNNDPIVTV 143

Qy 121 KKYFQGIYDVLQEGYSDCAMEIVRVMRALVTSTLQKRLTMGGLNSP 172
 Db 144 KRYFQGIYDVLQEGYSDCAMEIVRVMRALVTSTLQKRLTMGGLNSP 195

[illegible]

DT	01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE	PoIfn-alpha II-3 protein precursor.
GN	Name=PoIfn-alpha II-3;
OS	Sus scrofa (pig).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX	NCBI_TaxID=9823;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=domestica; TISSUE=liver;
RX	MEDLINE=92193689; PubMed=1800582;
RA	Leffevre F., La Bonnardiere C., Mege D.;
RT	"The porcine family of interferon-omega cloning, structural analysis
RL	and functional studies of five related genes.";
RL	J. Interferon Res. 11:341-350(1991).
CC	-1- SIMILARITY: Belongs to the alpha/beta interferon family.
DR	EMBL; X57194; CAA04080.1; -.
DR	PIR; S23712; S23712.
DR	HSSP; P56828; 1B5L.
DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR	GO; GO:0006952; P:defense response; IEA.
DR	InterPro; IPR009079; 4 helix cytokine.
DR	InterPro; IPR000471; Interferon_abd.
DR	Pfam; PF00143; Interferon_1
DR	PRINTS; PRO0266; INTERFERONAB.
DR	Prodom; P0000550; Interferon_abd; 1.
DR	SMART; SM00076; IFabd; 1.
DR	PROSITE; PS00252; INTERFERON_A_B; 1.
KW	Antiviral; Cytokine; Signal.
FT	SIGNAL 1 23 Potential.
FT	CHAIN 24 190 Interferon-alpha II-3.
SO	SEQUENCE 190 AA; 21535 MW; 1AF9321B845B397 CRC64;
Query Match	53.9%; Score 488.5; DB 2; Length 190;
Best Local Similarity	59.6%; Pred. No. 2.5e-37;
Matches 102; Conservative 23; Mismatches 41; Indels 5; Gaps 1;	
CY	1 CYLSRKMLDRLREKLKLLDRNNRSLSPSSCLQDRKDFGLPOEWMVGDDLOKQAFPYLYEM 60
DB	24 CDLSQNHNVGRKVLVLHQRRSLSPSPCLDKRDFGFPQEMVGSQLOKQALSLVHEM 83
CY	61 LQGSFNFYTESHSAAADDTLLLEDTCTGLQOQLDHLPTCRGQWGEEDSELGNDPIVTV 120
DB	84 LQGFLLHLHTRSSAANDSTLLDXTLDCGLHQLEDDLPCLVQEMEGQSAAG-----MAV 138
CY	121 KKRYQGIYDIYQEKGYSDCAEIVYEMRALTIVSTTLQKRLITMGGLNS 171
DB	139 KRYEGIHLYLKEKIVSDCAEYIVREIVTRELSTLYLQERTLIQANVLDGS 189
RESULT 39	
ID	IN01_HUMAN
AC	P05000;
DT	13-AUG-1987 (Rel. 05, Created)
DT	01-JUL-1993 (Rel. 26, Last sequence update)
DT	25-OCT-2004 (Rel. 45, Last annotation update)
DE	Interferon omega-1 precursor (Interferon alpha-II-1).
GN	Name=IFNM1;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=85187974; PubMed=2985369;
RA	Capon D.V., Shepard H.W., Goeddel D.V.;
RT	"Two distinct families of human and bovine interferon-alpha genes are
RT	coordinately expressed and encode functional polypeptides.";
RL	Mol. Cell. Biol. 5:768-779(1985).


```

RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Leukocyte; PubMed=1647209; DOI=10.1016/0167-4781(91)90004-6;
RX MEDLINE=91273345; PubMed=1647209; DOI=10.1016/0167-4781(91)90004-6;
RA Adolf G.R., Fruehbeis B., Hauptmann R., Kalener I., Maurer-Fogy I.,
  Oestermann E., Patzelt E., Schwendenwein R., Sommergruber W.,
  Zoepfel A.,
RT "Human interferon omega 1: isolation of the gene, expression in
  Chinese hamster ovary cells and characterization of the recombinant
  protein.",
RL Biochim. Biophys. Acta 1089:167-174(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feringold E.A., Grouse L.H., Derge J.G.,
  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
  Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
  Brownstein W.J., Ueda T.B., Toshiyuki S., Carrincci P., Prange C.,
  Raha S.S., Loquiano N.A., Peters G.J., Abdramon R.D., Mullaly S.J.,
  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
  Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
  Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
  Fehey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
  Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
  Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
  Rodriguez Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
  Butcherfield A.C., Krzywinski M.I., Skalska U., Smallus D.E.,
  Schenck A., Schenck J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
  and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 22-195 FROM N.A.
RX MEDLINE=85269605; PubMed=3895159;
RA Hauptmann R., Sweetly P.,
RT "A novel class of human type I interferons.",
RL Nucleic Acids Res. 13:4739-4749(1985).
RN [5]
RP SEQUENCE OF 22-36.
RX PubMed=15340161; DOI=10.1110/pb.04682504;
RA Zhang Z., Henzel W.J.,
RT "Signal peptide prediction based on analysis of experimentally
  verified cleavage sites.",
RL Protein Sci. 13:2819-2824(2004).
RN [6]
RP SEQUENCE OF N-TERMINUS, AND CARBOHYDRATE-LINKAGE SITE.
RX MEDLINE=50264422; PubMed=1693148;
RA Adolf G.R., Maurer-Fogy I., Kalener I., Cantell K.,
RT "Purification and characterization of natural human interferon omega
  1. Two alternative cleavage sites for the signal peptidase.",
RL J. Biol. Chem. 265:9290-9295(1990).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.1sb-61b.ch/announce/
  or send an email to license@sb-61b.ch).
CC EMBL: M11003; AAA52724.1; -
CC EMBL: X58822; CAA41626.1; -
CC EMBL: BC069095; AAH69095.1; -
CC EMBL: X02669; CAA26501.1; -
CC EMBL: A12140; CAA01011.1; -
CC PIR: A93070; IWHU1.
CC HSP: P01563; IITF.
CC Glycosubsteds: P05000; -.

```

```

DR Genew; HGNC:5448; IFN1.
DR MIM; 147553; -.
DR GO; GO:0005126; F:hematopoietic/interferon-class (D200-domain. . .; TAS.
DR GO; GO:0007050; P:cell cycle arrest; TAS.
DR GO; GO:0009615; P:response to virus; TAS.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR004771; Interferon_abd.
DR Pfam; PF00143; Interferon_1.
DR PRINTS; PR00266; INTERFERONAB.
DR PRODOM; PD000550; Interferon_abd.1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
DR Antiviral; Cytokine; Direct protein sequencing; Glycoprotein;
  MultiGene family; Signal.
FT SIGNAL 1 23
FT CHAIN 1 195
FT DISULFID 24 122
FT DISULFID 52 162
FT CARBOHYD 101
FT FTID 111
FT CONFLICT 111 111
SQ SEQUENCE 195 AA; 22319 MW; 1B4306F3487987FA CRC64;
  Query Match 52.1%; Score 473; DB 1; Length 195;
  Best Local Similarity 55.6%; Pred. No. 7e-36;
  Matches 95; Conservative 28; Mismatches 48; Indels 0; Gaps 0;
  1 CYLSRKMLDARENILKLDNRNRLSPHSCLDRKDFGLPEWVBDQLQKDAFPVLYEM 60
  24 CDLPQNGGLSLRMTVLVLLHQRRISPLCLKDRDPFPFGVMVGSGLQKXHVMSVLHEM 83
  61 LQGSFNFPTREHSAANDTTLLEOLCTGLOOQDLHDLTCRGQVNGEEDSELGNMDDIVTV 120
  84 LQGFSLFHTERSAANMTLLDQLHTGLHQQLHTLTCLLQVVGESASACISSPALTL 143
  121 KKYPQGIYDYLQEKSGDCAWEIVREVMRALTVSTLQKRLTGMGDLNS 171
  144 RRYFGIRVYLKRGKYSDCAMEVVRMIMKSLFSTMGERTLRKSDLLGS 194
  RESULT 40
  ID 029084 PRELIMINARY; PRT; 179 AA.
  AC 029084;
  DT 01-NOV-1996 (TREMURel. 01, Created)
  DT 01-NOV-1996 (TREMURel. 01, Last sequence update)
  DT 01-MAR-2004 (TREMURel. 26, Last annotation update)
  DE PoIFN-alpha II-4 protein precursor.
  GN Name=PoIFN-alpha II-4;
  OS Sue secreta (Pig).
  OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
  OC NCBI_TaxID=9823;
  RN [1]
  RP SEQUENCE FROM N.A.
  RC STRAIN=domestic; TISSUE=liver;
  RX MEDLINE=92193689; PubMed=1800582;
  RA Lettreve F., La Bonnardiere C., Mege D.,
  RT "The porcine family of interferon-omega: cloning, structural analysis
  and functional studies of five related genes.",
  RL J. Interferon Res. 11:341-350(1991).
  CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
  CC EMBL: X57195; CAA40481.1; -
  CC PIR: S23710; S23710.
  CC HSP: P56828; IBSL.
  DR GO; GO:0005576; C:extracellular; IEA.
  DR GO; GO:0005126; F:hematopoietic/interferon-class (D200-domain. . .; IEA.
  DR GO; GO:0006952; P:defense response; IEA.
  DR InterPro; IPR009079; 4_helix_cytokine.
  DR InterPro; IPR004771; Interferon_abd.
  DR Pfam; PF00143; Interferon_1.
  DR PRINTS; PR00266; INTERFERONAB.
  DR PRODOM; PD000550; Interferon_abd.1.
  DR SMART; SM00076; Ifabd; 1.

```



```

DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KM Antiviral; Cytokine; Signal. Potential.
FT CHAIN 1 23
FT SIGNAL 24 179
SQ SEQUENCE 179 AA; 20621 MW; 7D5D2ED05ABF0AD CRC64;

Query Match
Best Local Similarity 51.8%; Score 469.5; DB 2; Length 179;
Matches 95; Conservative 26; Mismatches 35; Indels 5; Gaps 1;

QY 1 CYLSRKMLDARENKLLDRNNRLSPHSCLQDRKDFGLPEQWVGDLQKQDAFPVLYEM 60
DB CDLFQNHVHSRKVLVLRQWRRLSPFCLKDRKDFPQPMVGSQLOKTOAIVSLHEM 83

QY 61 LQGSFNLFTYHSSAAMDITLLBOLCTGLQOQLDHLDTGCGQVNGEEDSELGNMIPVTV 120
DB LQGFLLHTHRSASAAWDTLLDLCGLHQHLEDSLCVQVGEQASALE-----MAV 138

QY 121 KKYPQGIYDYLQEKGYSDCAMEIVRVEEMRALTVSTTLQRLTKMGDDLNSP 161
DB 139 KRYFEGIHLYLKEKKYSDCAMEIVRVEIMRLSLSNMQR 179

RESULT 41
Q13168 PRELIMINARY; PRT; 174 AA.
ID 013168
AC 013168
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Interferon omega-1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=Chinese W1;
RA Zeng Q., Li M., Zhou Y., Guo H., Hou Y.;
RT "The cloning, sequencing of the primary structure and expression in E.
RT coli Chinese human IFN-W1 gene."
RL Sci. China, Ser. B, Chem. Life Sci. Earth Sci. 0:0-0(0).
RN 2
RP SEQUENCE FROM N.A.
RC STRAIN=Chinese W1;
RA Xu L.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
DR EMBL; U25670; AAA70091.1; -.
DR PIR; PC2204; PC2204.
DR HSP; P01563; IITP.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005126; F:hematicoprotein; Interferon-class (D200-domain. . .); IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon_1.
DR PRINTS; PR00266; INTERFERONAB.
DR PRODOM; PD000550; Interferon_abd.1.
DR SMART; SM00076; Ifabd.1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KM Antiviral; Cytokine.
FT NON TER 1
SQ SEQUENCE 174 AA; 20249 MW; B1CC9AB593016C5 CRC64;

Query Match
Best Local Similarity 50.9%; Score 462; DB 2; Length 174;
Matches 93; Conservative 26; Mismatches 50; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENKLLDRNNRLSPHSCLQDRKDFGLPEQWVGDLQKQDAFPVLYEM 60
DB CDLPQNHGLSRNTLVLLHQMRRISPLCLKDRDRDFPQPMVGSQLOKRAHVMASLHEM 62

```

```

QY 61 LQGSFNLFTYHSSAAMDITLLBOLCTGLQOQLDHLDTGCGQVNGEEDSELGNMIPVTV 120
DB LQGFLLHTHRSASAAWDTLLDLCGLHQHLEDSLCVQVGEQASALE-----MAV 138

QY 121 KKYPQGIYDYLQEKGYSDCAMEIVRVEEMRALTVSTTLQRLTKMGDDLNSP 171
DB 123 RRYFQGIYVLYLKEKKYSDCAMEIVRVEIMRLSLSNMQR 173

RESULT 42
INOT HORSE
ID INOT HORSE STANDARD; PRT; 195 AA.
AC P05001;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 23-MAR-2004 (Rel. 43, Last annotation update)
DE Interferon omega-1 precursor (Interferon alpha-II-1).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN 1
RP SEQUENCE FROM N.A.
RC MEDLINE=87053170; PubMed=3022999;
RA Hämmler A., Hauptmann R., Adolf G.R., Swelly P.;
RT "Molecular cloning and expression in Escherichia coli of equine type I
RT interferons."
RL DNA 5:345-356(1986).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; M14544; AAA30955.1; -.
DR EMBL; A15991; CAA01259.1; -.
DR PIR; E24912; IYHO21.
DR HSP; P56828; IBSL.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon_1.
DR PRINTS; PR00266; INTERFERONAB.
DR PRODOM; PD000550; Interferon_abd.1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KM Antiviral; Cytokine; Glycoprotein; Multigene family; Signal.
FT CHAIN 1 23
FT DISULFID 24 195
FT DISULFID 24 122
FT DISULFID 52 162
FT CARBOHYD 101 101
SQ SEQUENCE 195 AA; 21882 MW; A81C3CF0A7CA9B8E CRC64;

Query Match
Best Local Similarity 49.0%; Score 444; DB 1; Length 195;
Matches 91; Conservative 26; Mismatches 55; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENKLLDRNNRLSPHSCLQDRKDFGLPEQWVGDLQKQDAFPVLYEM 60
DB CDLPASLDLRKQKTLVLLHQMRRISPLCLKDRDRDFPQPMVGSQLOKRAHVMASLHEM 83

QY 61 LQGSFNLFTYHSSAAMDITLLBOLCTGLQOQLDHLDTGCGQVNGEEDSELGNMIPVTV 120
DB LQGFLLHTHRSASAAWDTLLDLCGLHQHLEDSLCVQVGEQASALE-----MAV 143

QY 121 KKYPQGIYDYLQEKGYSDCAMEIVRVEEMRALTVSTTLQRLTKMGDDLNSP 172
DB 144 KRYFRRIRLYLTKKKYSDCAMEIVRVEIMRLSLSNMQR 195

```

```

RESULT 43
ID INAD HUMAN STANDARD; PRT; 189 AA.
AC P01570;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interferon alpha-5 precursor (Interferon alpha-G) (leif G) (Interferon
  alpha-61).
GN Name=IFNA5;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=86037205; PubMed=4057246;
  Henco K., Brosius J., Fujisawa A., Fujisawa J.-I., Haynes J.R.,
  Hochstadt J., Kovacic T., Pasak M., Schamboeck A., Schmid J.,
  Todokoro K., Waelchli M., Nagata S., Weissmann C.;
  "Structural relationship of human interferon alpha genes and
  pseudogenes";
  J. Mol. Biol. 185:227-260(1985).
RN [2]
RP SEQUENCE OF 57-189 FROM N.A.
RC TISSUE=Spleen;
  MEDLINE=81148795; PubMed=6163083;
  Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,
  McCandliss R., Seeburg P.H., Ullrich A., Yelveton E., Gray P.W.;
  "The structure of eight distinct cloned human leukocyte interferon
  cDNAs";
  Nature 290:20-26(1981).
RN [3]
RP SEQUENCE OF 22-36.
  MEDLINE=15340161; DOI=10.1110/ps.04682504;
  Zhang Z., Henzel W.J.;
  "Signal peptide prediction based on analysis of experimentally
  verified cleavage sites";
  Protein Sci. 13:2819-2824(2004).
CC -1- FUNCTION: Produced by macrophages, IFN-alpha have antiviral
  activities. Interferon stimulates the production of two enzymes: a
  protein kinase and an oligoadenylate synthetase.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X02956; CAA26702.1; -
DR EMBL; V00541; CAA23802.1; -
DR PIR; S43716; IYHUA7.
DR HSSP; P01563; 11TF.
DR Genew; HGNC:5426; IFNA5.
DR MIM; 147565; -
DR GO; GO:0005116; F:hematopoietin/interferon-class (D200-domain. . .; TAS.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR PRODOM; PD000550; Interferon abd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine; Direct protein sequencing; Multigene family;
  Signal.
FT SIGNAL 1 21
FT CHAIN 22 189 Interferon alpha-5.
FT DISULFID 24 122 By similarity.
FT DISULFID 52 162 By similarity.

```

```

SQ SEQUENCE 189 AA; 21942 MW; C605992FE2E78043 CRC64;
Query Match 48.5%; Score 440; DB 1; Length 189;
Best Local Similarity 53.0%; Pred. No. 7.8e-33;
Matches 87; Conservative 28; Mismatches 49; Indels 0; Gaps 0;

OY 1 CYLSRKMLDARENLKLDNRNRLSPHSCLDRDPGLPGEMVSGDQGXQOAPFVLYEM 60
  |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 24 CDLPQTHLSNRRLTMAQNGRISPSCLDRDHFGRPOEEFGNGCFQKQAISVLHEM 83
  |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 61 LQSFNLFYTHSSAAMDITLLDQLCTGLQOQLDHLDTCRGQWGEEDSELGNDPIYTV 120
  |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 84 IQQTFNLFSTQSSATNDETLIDKFYTELYQLNDLEACMQWGEVDETPLMANDSILTV 143
  |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 121 KRYFGIYDYLQEKGYSDCAEIVVENMRALVTSTLQKRLTK 164
  |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 144 RKYFORITLYLTERKYSFCAMEVVAEIMRSFSLANLQERLRR 187
  |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 44
ID INAD HUMAN STANDARD; PRT; 189 AA.
AC P01570;
DT 21-JUL-1986 (Rel. 01, Created)
DT 05-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interferon alpha-14 precursor (Interferon alpha-H) (leif H)
  (Interferon lambda-2-H).
GN Name=IFNA14;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
  MEDLINE=86037205; PubMed=4057246;
  Henco K., Brosius J., Fujisawa A., Fujisawa J.-I., Haynes J.R.,
  Hochstadt J., Kovacic T., Pasak M., Schamboeck A., Schmid J.,
  Todokoro K., Waelchli M., Nagata S., Weissmann C.;
  "Structural relationship of human interferon alpha genes and
  pseudogenes";
  J. Mol. Biol. 185:227-260(1985).
RN [2]
RP SEQUENCE FROM N.A.
  MEDLINE=81201124; PubMed=6165082;
  Lawn R.M., Adelman J., Dull T.J., Gross M., Goeddel D.V., Ullrich A.;
  "DNA sequence of two closely linked human leukocyte interferon
  genes";
  Science 212:1159-1162(1981).
RN [3]
RP SEQUENCE FROM N.A.
  MEDLINE=81148795; PubMed=6163083;
  Goeddel D.V., Leung D.W., Dull T.J., Gross M., Lawn R.M.,
  McCandliss R., Seeburg P.H., Ullrich A., Yelveton E., Gray P.W.;
  "The structure of eight distinct cloned human leukocyte interferon
  cDNAs";
  Nature 290:20-26(1981).
RN [4]
RP SEQUENCE OF 24-53, AND CARBOHYDRATE-LINKAGE SITE ASN-95.
  MEDLINE=98087498; PubMed=9425112;
  Nyman T.A., Toeloe H., Parkkinen J., Kalkkinen N.;
  "Identification of nine interferon-alpha subtypes produced by Sendai
  virus-induced human peripheral blood leucocytes";
  Biochem. J. 329:295-302(1998).
RN [5]
RP ABSENCE OF POLYMORPHISM.
  MEDLINE=97067358; PubMed=8910771;
  Huessein M., Gill D.S., Liao M.-J.;
  "Identification of interferon-alpha 7, -alpha 14, and -alpha 21
  variants in the genome of a large human population.";
  J. Interferon Cytokine Res. 16:853-859(1996).
CC -1- FUNCTION: Produced by macrophages, IFN-alpha have antiviral
  activities. Interferon stimulates the production of two enzymes: a

```

```

CC protein kinase and an oligoadenylate synthetase.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk.)
-----
DR EMBL; V00533; CAA23794.1; -.
DR EMBL; X02959; CAA26705.1; -.
DR EMBL; V00542; CAA23803.1; -.
DR PIR; A92916; IYHU14.
DR HSSP; P01563; 1ITF.
DR GlycoSiteDB; P01570; -.
DR Genew; HGNC:5420; IFNA14.
DR MIM; 147579; -.
DR GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; TAS.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR00471; Interferon_abd.
DR Pfam; PF00143; Interferon_1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine; Direct protein sequencing; Glycoprotein;
KW Multigene family; Signal.
FT SIGNAL 1 23
FT CHAIN 24 189 Interferon alpha-14.
FT DISULFID 24 122 By similarity.
FT DISULFID 52 162 By similarity.
FT CARBOHYD 95 95 N-linked (GlcNAc. . .).
FT CONFLICT 175 175 L -> F (in Ref. 3).
SQ SEQUENCE 189 AA; 22062 MW; B6B71E2F0D644FE7 CRC64;
Query Match 48.5%; Score 440; DB 1; Length 189;
Best Local Similarity 54.9%; Pred. No. 7,8e-33;
Matches 90; Conservative 26; Mismatches 48; Indels 0; Gaps 0;
QY 1 CYLSRKLMLDARENIKLLDRNRRLSPHSCLDRKDFGLPQEMVEGDLQKQDAEPVLYEM 60
DB 24 CNLSQTSILNRRRTLMLAQMRRIISPFSCLKDRHDFEPQEPQNGQKQALSVLHEM 83
QY 61 LQGFNLFYTHSSAANDTLLLEQLCTGLQOQLHDLPTCRQWGESELSGNDDPIVTV 120
DB 84 MQQTFNLFSTKSSAAMDETLLEKRYIELFQQMNDLEACVIGEVETPLMDESDILAV 143
QY 121 KKYFGIYDYLQEGYSDCAMEIVREVMRALTVSTTLQKRLTK 164
DB 144 KKYQRITLYLMEKYSKPCAMEVYRAEIMRSLSTFNQKRLRR 187

```

```

RT genes."
RL Science 212:1159-1162(1981).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85229953; Pubmed=3891272;
RA Mizoguchi J., Pltha P.M., Raj N.B.K.;
RT "Efficient expression in Escherichia coli of two species of human
RL interferon-alpha and their hybrid molecules."
RL DNA 4:221-232(1985).
RN [3]
RP SEQUENCE OF 14-189 FROM N.A.
RX MEDLINE=85235859; Pubmed=4008999;
RA Lund B., von Gabain A., Edlund T., Ny T., Lundgren E.;
RT "Differential expression of interferon genes in a substrain of Namalwa
RL cells."
RL J. Interferon Res. 5:229-238(1985).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=87024453; Pubmed=3767336;
RA Savelliev V.I., Zlochevsky M.L., Sorokin A.V., Naroditskaya V.A.,
RA Bolotin A.P., Demjanova N.G., Kozlov Y.I., Neznanov N.S.,
RA Gazaryan K.G., Monastyrskaya G.S., Sverdlov E.D.;
RT "Cloning and the determination of the nucleotide sequences in 2 genes
RL of human leukocyte interferons."
RL Anticlot. Med. Biotechnol. 31:592-596(1986).
RN [5]
RP SEQUENCE OF 24-58.
RX MEDLINE=86087498; Pubmed=9425112;
RA Nyman T.A., Toeloe H., Parkkinen J., Kalkkinen N.;
RT "Identification of nine interferon-alpha subtypes produced by Sendai
RL virus-induced human peripheral blood leucocytes."
RL Biochem. J. 329:295-302(1998).
RN [6]
RP VARIANT ARG-184.
RX MEDLINE=98376207; Pubmed=9712362;
RA Hussain M., Tan T., Ni D., Gill D.S., Liao M.-J.;
RT "A new allele of interferon-alpha17 gene encoding IFN-alpha17b is the
RL major variant in human population."
RL J. Interferon Cytokine Res. 18:469-477(1998).
CC -1- FUNCTION: Produced by macrophages, IFN-alpha have antiviral
CC activities. Interferon stimulates the production of two enzymes: a
CC protein kinase and an oligoadenylate synthetase.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk.)
-----
DR EMBL; M1026; AAA52725.1; -.
DR EMBL; V00532; CAA23793.1; -.
DR EMBL; M38289; AAA59165.1; -.
DR EMBL; M71246; AAA52713.1; -.
DR PIR; A01835; IYHU49.
DR PIR; I56314; I56314.
DR HSSP; P01563; 1ITF.
DR Genew; HGNC:5422; IFNA17.
DR MIM; 147583; -.
DR GO; GO:0005132; F:interferon-alpha/beta receptor binding; TAS.
DR GO; GO:0009615; P:response to virus; TAS.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR00471; Interferon_abd.
DR Pfam; PF00143; Interferon_1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine; Direct protein sequencing; Multigene family;
KW Polymorphism; Signal.
FT SIGNAL 1 23

```

```

FT CHAIN 24 189 Interferon alpha-17.
FT DISULFID 24 122 By similarity.
FT DISULFID 52 162 By similarity.
FT VARIANT 184 184 I->R.
FT CONFLICT 57 57 /FTID=VAR 013020.
FT CONFLICT 78 78 H->P (in Ref. 1).
FT SEQUENCE 189 AA; 21728 MM; 04486A9B9DFC32 CRC64;

Query Match
Best Local Similarity 55.5%; Pred. No. 1.2e-32;
Matches 91; Conservative 25; Mismatches 48; Indels 0; Gaps 0;

Oy 1 CYLSRKMLDARENLKLDNRNRLSPHSCLODRKDFGLPOEMVSGDQLQKQAPVLYEM 60
Db 24 CDLPQTHSLGNRRALILLAQMGRISSPFCCLKDRHDFGLPOEFPQGNOPKTOAISVLIEM 83

Oy 61 LQGSFNLPTHTSSAAMDPTLLLEQLCTGLQOQDLHLDTCRGQVNGEEDSEIGNMDPIVTV 120
Db 84 IQQTFNLFTSDSSAAMEQSLEKFTSTLYQQLNNLECVIQVGMETPLMNEDSLIAV 143

Oy 121 KKVEQGIYDYLQEKGYSDCAMEIYRVEMMRALTIVSTTLQKRLTK 164
Db 144 RKYFORITLYLTEKKYSCAMEIVRAEIMRSLSTTNLQKILRR 187

RESULT 46
O28562 PRELIMINARY; PRT; 195 AA.
ID Q28562;
AC Q28562;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ovine Interferon alpha precursor.
GN Name=amy 49;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Whaley A.E., Carroll R.S., Imakawa K.;
CC Submitted (APR-1991) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the alpha/beta Interferon family.
DR EMBL: X59068; CAA4191.1; -.
DR PIR: I46398; I46398.
DR HSPSP, P01563; ITTP.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO: GO:0006952; P:defense response; IEA.
DR InterPro: IPR009079; 4 helix cytokine.
DR InterPro: IPR000471; Interferon_abd.
DR Pfam: PF00143; Interferon_1.
DR PRINTS: PR00266; INTERFERONAB.
DR ProDom: PD000550; Interferon_abd; 1.
DR SMART: SM00076; IFabd; 1.
DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine; Signal.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 195 Ovine Interferon alpha.
SQ SEQUENCE 195 AA; 22006 MM; 388EE70C586A928 CRC64;

Query Match
Best Local Similarity 47.5%; Score 431; DB 2; Length 195;
Matches 54.3%; Pred. No. 5.6e-32;

```

```

Matches 88; Conservative 23; Mismatches 51; Indels 0; Gaps 0;

Oy 11 ARENLKLDNRNRLSPHSCLODRKDFGLPOEMVSGDQLQKQAPVLYEMIQSFNLYT 70
Db 34 SRSLTVLDDQWRVRSPVLCIKDRRDFQPREVNVGSGFQKQVTSVLHEMLQQLFNLHT 93

Oy 71 EHSSAAMDPTLLLEQLCTGLQOQDLHLDTCRGQVNGEEDSEIGNMDPIVTVKRYFGIYDY 130
Db 94 AHSSAAMNNTLLELHAALHQQQLGLTCLVQAMGEEDSVLTADSPFLMKRYFORILRY 153

Oy 131 LQEKGYSDCAMEIYRVEMMRALTIVSTTLQKRLTQVGGDLSNP 172
Db 154 LDEKHSGCAMELYRMEIRRAFSTADLQESLRKQDILASP 195

RESULT 47
O28844 PRELIMINARY; PRT; 195 AA.
ID Q28844;
AC Q28844;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interferon-omega48.
DE Interferon-omega48.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=94132653; PubMed=8301151;
RA Charlier M., L'Hardon R., Boissard M., Matral J., Gaye P.;
RT "Cloning and structural analysis of four genes encoding Interferon-omega in rabbit."
RL J. Interferon Res. 13:313-322(1993).
CC -1- SIMILARITY: Belongs to the alpha/beta Interferon family.
DR EMBL: S68929; AAC60525.2; -.
DR HSPSP, P56828; IBSL.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO: GO:0006952; P:defense response; IEA.
DR InterPro: IPR009079; 4 helix cytokine.
DR InterPro: IPR000471; Interferon_abd.
DR Pfam: PF00143; Interferon_1.
DR PRINTS: PR00266; INTERFERONAB.
DR ProDom: PD000550; Interferon_abd; 1.
DR SMART: SM00076; IFabd; 1.
DR PROSITE: PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine.
SQ SEQUENCE 195 AA; 21981 MM; D4D2E3EF5134A5SF CRC64;

Query Match
Best Local Similarity 47.4%; Score 430; DB 2; Length 195;
Matches 88; Conservative 23; Mismatches 50; Indels 0; Gaps 0;

Oy 11 ARENLKLDNRNRLSPHSCLODRKDFGLPOEMVSGDQLQKQAPVLYEMIQSFNLYT 70
Db 34 SRSLTVLDDQWRVRSPVLCIKDRRDFQPREVNVGSGFQKQVTSVLHEMLQQLFNLHT 93

Oy 71 EHSSAAMDPTLLLEQLCTGLQOQDLHLDTCRGQVNGEEDSEIGNMDPIVTVKRYFGIYDY 130
Db 94 AHSSAAMNNTLLELHAALHQQQLGLTCLVQAMGEEDSVLTADSPFLMKRYFORILRY 153

Oy 131 LQEKGYSDCAMEIYRVEMMRALTIVSTTLQKRLTQVGGDLSNP 171
Db 154 LDEKHSGCAMELYRMEIRRAFSTADLQESLRKQDILASP 194

RESULT 48
ID INA4 HUMAN STANDARD; PRT; 189 AA.
AC P05014; P13358;
DT 13-AUG-1987 (Ref. 05, Created)
DT 13-AUG-1987 (Ref. 05, Last sequence update)

```

DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interferon alpha-4 precursor (Interferon alpha-4B) (Interferon alpha-
 DE M1) (Interferon alpha-76).
 GN Name=IFN4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=86037205; PubMed=4057246;
 RA Henko K., Brosius J., Fujisawa J.-I., Haynes J.R.,
 RA Hochstadt J., Kovacic T., Pasek M., Schambeck A., Schmid J.,
 RA Tokoro K., Waelchli M., Nagata S., Weissmann C.;
 RT "Structural relationship of human interferon alpha genes and
 RT pseudogenes.";
 RL J. Mol. Biol. 185:227-260 (1985).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=84307815; PubMed=6089830;
 RA Linane A.W., Bellharz M.W., McMullen G.L., Macreadie I.G., Murphy M.,
 RA Nieber I.T., Novitski C.E., Woodrow G.C.;
 RT "Nucleotide sequence and expression in E. coli of a human interferon-
 RT alpha gene selected from a genomic library using synthetic
 RT oligonucleotides.";
 RL Biochem. Int. 8:725-732 (1984).
 RN [3]
 RN SEQUENCE OF 24-56.
 RX MEDLINE=98087498; PubMed=9425112;
 RA Nyman T.A., Toeloe H., Parkkinen J., Kalkkinen N.;
 RT "Identification of nine interferon-alpha subtypes produced by Sendai
 RT virus-induced human peripheral blood leucocytes.";
 RL Biochem. J. 329:295-302 (1998).
 RN [4]
 RN POLYNORPHISM
 RX MEDLINE=97474410; PubMed=9335344;
 RA Hussain M., Gill D.S., Liao M.-J.;
 RT "Both variant forms of interferon-alpha4 gene (IFN4a and IFN4b) are
 RT present in the human population.";
 RL J. Interferon Cytokine Res. 17:559-566 (1997).
 CC -1- FUNCTION: Produced by macrophages, IFN-alpha have antiviral
 CC activities. Interferon stimulates the production of two enzymes: a
 CC protein kinase and an oligoadenylate synthetase.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- POLYNORPHISM: Two forms exist; alpha-4a and alpha-4b (shown here).
 CC They seem to be equally abundant.
 CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X02955; CAA26701.1; -;
 DR EMBL; M27318; AAA52726.1; -;
 DR PIR; E23753; IYHU4B;
 DR PIR; I52347; I52347;
 DR HSSP; P01563; IITF.
 DR Genew; HGNC:5425; IFN4.
 DR MIM; 147564; -;
 DR GO; GO:0005132; P:interferon-alpha/beta receptor binding; TAS.
 DR GO; GO:0009615; P:response to virus; TAS.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR00471; Interferon_abd.
 DR Pfam; PF00143; Interferon; 1.
 DR PRINTS; PR00266; INTERFERONAB.
 DR PRODOM; PD000550; INTERFERONAB.
 DR PROSITE; PS00252; INTERFERON_AB_D; 1.
 DR Antiviral; Cytokine; Direct protein sequencing; Multigene family;
 KW Polymorphism; Signal.

FT SIGNAL 1 23
 FT CHAIN 24 189 Interferon alpha-4.
 FT DISULFID 24 122 By similarity.
 FT DISULFID 52 162 By similarity.
 FT VARIANT 74 74 T->A (in alpha-4A).
 FT VARIANT 137 137 V->E (in alpha-4A).
 FT VARIANT 137 137 /FTid=VAR_013003.
 FT VARIANT 137 137 /FTid=VAR_013003.
 SQ SEQUENCE 189 AA; 21808 MW; 4198F9C8E2A80C CRC64;
 Query Match 47.3%; Score 429; DB 1; Length 189;
 Best Local Similarity 54.3%; Pred. No. 8.2e-32;
 Matches 89; Conservative 25; Mismatches 50; Indels 0; Gaps 0;
 QY 1 CYLSRLKMLAREKILKLDNRNLSPLSHCLQDRKDFGLPEQWEGDLOKQAFVLYEM 60
 DB 24 CDLPQTHSLGNRRALITLQAGRIHSFSCAKDRHDFEPEEPDGHOFQTOALSVLHEM 83
 QY 61 LQGSFNLPTTHSSAAWDTTLLEQLCTGLQQQLDHLDTCRGQVMEEDSEIGNDPVTV 120
 DB 84 IQQTFNLFSTRDSSAAWEGSLBEFSTELVQQLNDLEACVIOEGVEETPLMNVDSILAV 143
 QY 121 KKTFQGIYDYLOEKGSDCMEIVRYVEMRALVSTTLQKRLTK 164
 DB 144 RKYFORITLYLTKKXSPCAMEVVRMRSLSTFWLQKRLRR 187
 RESULT 49
 INNA HUMAN STANDARD; PRT; 189 AA.
 ID INNA HUMAN
 AC P01566;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interferon alpha-10 precursor (Interferon alpha-C) (Ielf C)
 DE (Interferon alpha-6L).
 GN Name=IFNA10;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=9148795; PubMed=6163083;
 RA Goeddel D.V., Leung P.W., Dull T.J., Gross M., Lawn R.M.;
 RA McCandless R., Seeburg P.H., Ullrich A., Yelverton E., Gray P.W.;
 RT "The structure of eight distinct cloned human leukocyte interferon
 RT cDNAs.";
 RL Nature 290:20-26 (1981).
 RN [2]
 RN SEQUENCE OF 24-53.
 RX MEDLINE=98087498; PubMed=9425112;
 RA Nyman T.A., Toeloe H., Parkkinen J., Kalkkinen N.;
 RT "Identification of nine interferon-alpha subtypes produced by Sendai
 RT virus-induced human peripheral blood leucocytes.";
 RL Biochem. J. 329:295-302 (1998).
 CC -1- FUNCTION: Produced by macrophages, IFN-alpha have antiviral
 CC activities. Interferon stimulates the production of two enzymes: a
 CC protein kinase and an oligoadenylate synthetase.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; V00551; CAA23812.1; -;
 DR PIR; A60937; IYHUAS.
 DR HSSP; P01563; IITF.

```
DR Genew; HGNC:5418; IFNA10.
DR MIM; 147577; -.
DR GO; GO:0005376; C:extracellular; NAS.
DR GO; GO:0005132; F:Interferon-alpha/beta receptor binding; ISS.
DR GO; GO:0009615; P:response to virus; ISS.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine; Direct protein sequencing; Multigene family;
KW Signal.
FT SIGNAL 1 23
FT CHAIN 24 189 Interferon alpha-10.
FT DISULFID 24 122 By similarity.
FT DISULFID 52 162 By similarity.
SQ SEQUENCE 189 AA; 21835 MW; CEC68096FDA7068 CRC64;

Query Match 47.3%; Score 429; DB 1; Length 189;
Best Local Similarity 54.3%; Pred. No. 8.2e-32;
Matches 89; Conservative 26; Mismatches 49; Indels 0; Gaps 0;

QY 1 CYLSRKMLDARENLKILDRMNRSLSPHSCLODRKDFGLPOEMVGGDLOKQDAFPVLYEM 60
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 24 CDLPQTHSLGKRRRLILGQKGRISPSCLDRHDFRIPQEEFDGNOFQKAPALSVLHEM 83
   :|||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 61 LQGSFNLFTYEHSSAAMDITLLEQLCTGLQQQLDHLDTCRGQVNGEEDSBLGNMPTIVTV 120
   :|||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 84 IQQTFNLFSTKSSAAMDEDLDFKCTEIVYQQLNDLEACVQEVGVETPLMNDSDILAV 143
   :|||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 121 KKYFGIYDYLQEKGYSDCANEIVREMRALTYSTTLQKRLTK 164
   :|||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 144 RKYFORITLYLERKYSPCAEVVRAEIMRSLSTYNLQKRLRR 187
   :|||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

RESULT 50
Q9UMJ3 PRELIMINARY; PRT; 166 AA.
AC Q9UMJ3;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE IFNA protein (Fragment).
GN Name=IFNA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83299241; PubMed=6310510;
RA Weber H., Weissmann C.;
RT "Formation of genes coding for hybrid proteins by recombination
   between related, cloned genes in E. coli.";
RL Nucleic Acids Res. 11:5661-5669(1983).
CC -1- SIMILARITY: Belongs to the alpha/beta interferon family.
DR EMBL; M29884; AA52714.1; -.
DR PIR; H42753; H42753.
DR HSSP; P01563; 1ITF.
DR GO; GO:0005376; C:extracellular; IEA.
DR GO; GO:0005132; F:hematopoietin/interferon-c class (D200-domain. . .; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR InterPro; IPR009079; 4 helix_cytokine.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; Ifabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine.
FT NON_TER 1
SQ SEQUENCE 166 AA; 19386 MW; 4152EA2A78361BB8 CRC64;
```

```
Query Match 47.2%; Score 428; DB 2; Length 166;
Best Local Similarity 53.9%; Pred. No. 8.7e-32;
Matches 90; Conservative 24; Mismatches 47; Indels 6; Gaps 2;

QY 1 CYLSRKMLDARENLKILDRMNRSLSPHSCLODRKDFGLPOEMVGGDLOKQDAFPVLYEM 60
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1 CDLPETHSLDRRTTLLAQMSRISPSCLMDRHFDPQEEFDGNOFQKAPALSVLHEM 60
   :|||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 61 LQGSFNLFTYEHSSAAMDITLLEQLCTGLQQQLDHLDTCRGQVNGEEDSBLGNMPTIVTV 117
   :|||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 61 IQQTFNLFSTKSSAAMDEDLDFKCTEIVYQQLNDLEACVQEVGVETPLMNDSDILAV 117
   :|||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 118 VTKYFGIYDYLQEKGYSDCANEIVREMRALTYSTTLQKRLTK 164
   :|||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 118 LAVKVFRRITLYLERKYSPCAEVVRAEIMRSLSTYNLQKRLRR 164
   :|||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

Search completed: October 5, 2005, 10:38:16
Job time : 230 secs
```

THIS PAGE BLANK (USPTO)